

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2002, 11:03:09 ; Search time 3842.15 Seconds
(without alignments)
1807.663 Million cell updates/sec

Title: US-09-394-745-6489
Perfect score: 421
Sequence: 1 ggggccagcagcggtccggc.....ctcgacaagatctaaggggg 421

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
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22: em_pat:*
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25: em_ro:*
26: em_sts:*
27: em_sy:*

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28: em_un:*
29: em_vi:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB	ID	Description
No.	Score	Match	Length				
1	212	50.4	163055	2	AP003626	AP003626	Oryza sat
2	212	50.4	165909	2	AP003711	AP003711	Oryza sat
3	96.4	22.9	1031	8	AF139499	AF139499	Prunus ar
4	91.8	21.8	105807	8	AC006085	AC006085	Arabidops
5	90.4	21.5	844	8	AF140722	AF140722	Oryza sat
c 6	86.4	20.5	165873	2	AC090871	AC090871	Oryza sat
c 7	84.4	20.0	136198	2	AP003883	AP003883	Oryza sat
8	81.6	19.4	871	8	PHVPVPR3A	M75856	P.vulgaris
9	79.6	18.9	165873	2	AC090871	AC090871	Oryza sat
c 10	78.4	18.6	151085	8	AP003239	AP003239	Oryza sat
11	78.4	18.6	151100	8	AP003453	AP003453	Oryza sat
c 12	78.4	18.6	159497	2	AP003288	AP003288	Oryza sat
13	72.6	17.2	871	8	AY042871	AY042871	Arabidops
14	72.6	17.2	100028	8	ATF3C22	AL353912	Arabidops
15	69.2	16.4	21200	8	AP002044	AP002044	Arabidops
c 16	69.2	16.4	105768	8	AC069474	AC069474	Arabidops
c 17	67	15.9	118374	8	AC025416	AC025416	Genomic s
18	64.4	15.3	1382	9	BC011018	BC011018	Homo sapi
19	64.4	15.3	2273	9	AF062347	AF062347	Homo sapi
20	64.4	15.3	2347	9	AK025782	AK025782	Homo sapi
21	64.4	15.3	2418	9	AF062346	AF062346	Homo sapi
22	63.2	15.0	1621	3	AB001773	AB001773	Ciona sav
23	62.6	14.9	2167	10	AF062071	AF062071	Mus muscu
24	61.4	14.6	1279	8	AF361575	AF361575	Arabidops
25	61.4	14.6	2368	10	MMU251508	AJ251508	Mus muscu
26	61.4	14.6	107600	8	ATF16J13	AL049638	Arabidops
27	61.4	14.6	190026	8	ATCHRIV33	AL161533	Arabidops
28	61	14.5	528	8	AF325093	AF325093	Arabidops
29	60.6	14.4	1197	6	AR044461	AR044461	Sequence
30	60.6	14.4	1451	9	HSA251095	AJ251095	Homo sapi
31	60.6	14.4	1492	9	AF261138	AF261138	Homo sapi
32	60.6	14.4	1535	10	BC010683	BC010683	Mus muscu
33	60.6	14.4	1613	9	AF061739	AF061739	Homo sapi
34	60.6	14.4	1709	9	BC005283	BC005283	Homo sapi
c 35	59.6	14.2	89350	8	ATT12H17	AL021635	Arabidops
c 36	59.6	14.2	139316	8	ATF7H19	AL031018	Arabidops
c 37	59.6	14.2	193550	8	ATCHRIV58	AL161558	Arabidops
38	59	14.0	1512	6	AX086051	AX086051	Sequence

	39	59	14.0	1512	9	HSM801572	AL136598 Homo sapi
c	40	57.4	13.6	105689	8	AC005824	AC005824 Arabidops
	41	56.2	13.3	76042	8	AC006921	AC006921 Arabidops
	42	56.2	13.3	198944	8	ATCHRIV38	AL161538 Arabidops
	43	56.2	13.3	200576	8	ATFCA0	Z97335 Arabidopsis
	44	48.6	11.5	11019	9	AF062072	AF062072 Homo sapi
	45	48.6	11.5	162985	9	AL135924	AL135924 Human DNA

ALIGNMENTS

RESULT 1

AP003626

LOCUS AP003626 163055 bp DNA HTG 18-MAY-2001

DEFINITION Oryza sativa chromosome 6 clone P0429G06, *** SEQUENCING IN PROGRESS ***, in ordered pieces.

ACCESSION AP003626

VERSION AP003626.1 GI:14141687

KEYWORDS HTG; HTGS_PHASE2.

SOURCE Oryza sativa (cultivar:Nipponbare) DNA, clone:P0429G06.

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (sites)

AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.

TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0429G06

JOURNAL Published Only in DataBase (2001) In press

REFERENCE 2 (bases 1 to 163055)

AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

COMMENT NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

FEATURES Location/Qualifiers

source 1. .163055
/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="6"
/clone="P0429G06"

BASE COUNT 47965 a 33832 c 33488 g 47470 t 300 others

ORIGIN

Query Match 50.4%; Score 212; DB 2; Length 163055;
 Best Local Similarity 77.3%; Pred. No. 1.1e-38;
 Matches 310; Conservative 0; Mismatches 81; Indels 10; Gaps 4;

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Qy      19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgatgaacggcagcgacgc 78
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Db 122931 GCAGGAGCAGGCCAAGCTGGCAGCCTCCTCTATCGACAGCATTGTCAATGGTGGTGATTC 122990

Qy      79 cgtcatggagccggttgttgcctggcagcaacacggtagtagctgttgcccaagttgagtt 138
          || | ||| || || ||||| | || | | ||||| ||||| ||||| |||||
Db 122991 CGGGAAGGAACCAATTATTGCTG---GTCACGCTGAAGTAGCTGTTGCTCAAGTCGAGGT 123047

Qy     139 gcaaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggtggcggc 198
          | | || | || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 123048 GAAGAC---GCTTGTGTCGCAGCCTGCTGAGATTGCTGGTCCTAGTGAGGGGGTCACGGT 123104

Qy     199 gatctccaaaggggggaaggtangggccgaaccgggtgcagcgccctgcaggaagagggttgg 258
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Db 123105 GAACCCCAA---GGGGAGGGAAGGACCAATCGGTGCTCCACTTGTCGGAAGAGGGTTGG 123161

Qy     259 acttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccga 318
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Db 123162 TCTTACCGGATTCAACTGCCGATGTGGCAACTGTACTGCGCAATGCACCGCTATTCCGA 123221

Qy     319 caagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaagggcta 378
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 123222 TAAGCATGACTGCCAGTTTACTATCGGACCGCTGCTAGGGATGCTATTGCCAA-GGCTA 123280

Qy     379 atccggtggtgaaggcagacaagctcgacaagatctaagg 419
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RESULT 2
 AP003711
 LOCUS AP003711 165909 bp DNA HTG 31-MAY-2001
 DEFINITION *Oryza sativa* chromosome 6 clone P0417G12, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
 ACCESSION AP003711
 VERSION AP003711.1 GI:14270111
 KEYWORDS HTG; HTGS_PHASE2.
 SOURCE *Oryza sativa* (cultivar:Nipponbare) DNA, clone:P0417G12.
 ORGANISM *Oryza sativa*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; *Oryza*.
 REFERENCE 1 (sites)
 AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
 TITLE *Oryza sativa* nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0417G12
 JOURNAL Published Only in DataBase (2001) In press
 REFERENCE 2 (bases 1 to 165909)
 AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAY-2001) Takuji Sasaki, National Institute of


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RESULT      3
AF139499
LOCUS       AF139499      1031 bp      mRNA                      PLN          10-JUN-1999
DEFINITION  Prunus armeniaca p85RF mRNA, complete cds.
ACCESSION   AF139499
VERSION     AF139499.1   GI:5031280
KEYWORDS    .
SOURCE      apricot.
  ORGANISM  Prunus armeniaca
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Rosales; Rosaceae; Prunus.
REFERENCE   1 (bases 1 to 1031)
  AUTHORS   Mbeguie-A-Mbeguie,D. and Fils-Lycaon,B.R.
  TITLE     Molecular cloning and nucleotide sequence of a putative protein
            from apricot (Prunus armeniaca var. Bergeron)
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1031)
  AUTHORS   Mbeguie-A-Mbeguie,D. and Fils-Lycaon,B.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAR-1999) INRA, Domaine de Duclos, Petit-Bourg 97170,
            France
FEATURES             Location/Qualifiers
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                     /codon_start=1
                     /product="unknown"
                     /protein_id="AAD38146.1"
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                     ANPVVKAADKLEKI"
BASE COUNT      270 a      185 c      254 g      322 t
ORIGIN

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Db 306 GCAATGGAAATGAACCTGTTGTTGCTGCTGGTGTGGATGTTCAAGCCCATCTGGTGGAGC 365

Qy 141 aaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggtggcggcga 200
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Db 366 CAAAACTATCTCTTTACAACCATCCTTTTCCTTTGGTTCAGGTTTCAGGAGGGAGTGGTG 425

Qy 201 tctccaaaggggggaaggtangggccgaaccggtgcagcgccctgcaggaagaggggttgac 260
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Db 426 AGGCAAA-----GCCAGAAGGCCCAAACGTTGCGGAACCTTGCAACAAGAGAGTTGGAT 479

Qy 261 ttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccgaca 320
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Db 480 TAACAGGGTTCAATTGTCTGGTGTGGTCACCTTTTCTGTGCAGTACATCGTTATTTCAGACA 539

Qy 321 agcacgactgcaagttcgactaacggactgctgccaaaggacgccattgccaaagggcta 380
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Db 540 AACATGACTGCCCTTATGATTACCACACTGCTGCACGCGATGTGATTGCTAA-AGCCAAC 598

Qy 381 ccggtggtgaaggcagacaagctcgacaagatctaag 417
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Db 599 CCTGTTGTAAAGGCTGATAAGCTTGAAAAAATCTAAG 635

RESULT 4

AC006085

LOCUS AC006085 105807 bp DNA PLN 17-MAY-1999

DEFINITION Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence.

ACCESSION AC006085

VERSION AC006085.1 GI:4165340

KEYWORDS HTG.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 105807)

AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vysotskaia,V.S., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 105807)

AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.

TITLE Direct Submission

JOURNAL Submitted (03-DEC-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

REFERENCE 3 (bases 1 to 105807)

AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,

Lueros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V.,
 Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-1999) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 REFERENCE 4 (bases 1 to 105807)
 AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
 Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P.,
 Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,
 Lueros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V.,
 Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (17-MAY-1999) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 COMMENT On Jan 21, 1999 this sequence version replaced gi:4079615.
 BAC F11M15 is near molecular marker m280 on Chromosome I.
 e-mail for correspondence: arab@sequence.stanford.edu
 Genes with similarity to proteins in the databases are described as
 'putative', '-like' or 'similar to'. Genes that have EST
 similarity but no significant protein similarity are described as
 'unknown proteins'. Genes that are annotated based only on gene
 prediction software are described as 'hypothetical proteins'.
 The software programs used to predict genes include: Grail
 (Informatics Group, Oak Ridge National Laboratory,
<http://compbio.ornl.gov/section/index.html>), GENSCAN (Chris Burge,
<http://gnomic.stanford.edu/~chris/GENSCANW.html>), Fexa (V.Solovyev
 & A.Salamov, Sanger Centre, <http://genomic.sanger.ac.uk/>), and
 NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
 Denmark,<http://www.cbs.dtu.dk/NetPlantGene.html>).
 FEATURES Location/Qualifiers
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 /chromosome="I"
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gene      15856..18162
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EPAPVTPKGPKKMVKVIMGGSKLFRDSVSAIKQHERKVVPVAKRPKTNQIDCPEISF
SEEETSDLDKPHDDALVISLVDVGNEVQVRVLIDTGSSVDLIFLDTLVRMGISKKDIKG
ALSPLVSFTSETSMLLRTITLPVTAQGIVKMIETVFDPAAYNIILGTPWLYEMKAV
PSTYHQCCKFPTPTGVKQILGSQRTSRIVGEMTGISTEVISHELNVDPFTFKPVKQKYR
KLGPDRAEAVNAEVVRLLEEGLIREVKYPEWLANPVVVKKNGKWRVCVDFTDLNKAC
PKDCFPLPHIDRHVESTTGHEMLSFMDAFSAYNQILMNPDDQEKTSFITERGTYSKI
SSAKQWRFISTTCEFLGYIVTERGIEANPRQINAFAMSSPRTISEVRLTGRVAALN
SAVSSVLVRVERSDEPIFYVSKSFSDAETRYPMMEKLALAVVTSARKLRPYFQSHPI
VVLTSPLPLRAILHSPSQSGRLAKWAIELSEFDLEFRARTSLKSQVLAFLIELPLATA
ESDVPSQPWILHVDGASSKQSGAGVRLKLPTEVLEQSFRLAFNASNNEAEYESLLA
GLRLAIGVGVRLAQHCDSQLVASQYSGDYEAKDSRMEAYLDQETNFVTTTRAMRRRLD
EKAGSPEPQQPDDGDDSPFVPPVAEDEVPITDNPEVSNQIPHWDGADWREPIRNYIL
HGVLPDPKWAARKLKATNARFCIANDILYRRLISAPDAICIFGEQPRTVIKKIHDGTC
GNHSGGRSLAFKVKYGYFWPTMMADCEAYARRCEQCQKHAPYILQPAELLTSVSAPY
PYMKWSMDIIGPLHVSTRGVRFLVLTDYFSKWKAATYSNITQVQVRAFIWKEIICR
HGLPYEIVTDNGPQFISKHFESLCVRRQPVLWV"
gene 30507. .32896
      /gene="F11M15.6"
CDS   join(30507. .30946,31035. .31117,31386. .31474,31572.
.31645,
      31770. .31897,32160. .32896)
      /gene="F11M15.6"
      /note="Hypothetical protein; protein contains ethylene
      responsive element binding protein signature motif"
      /codon_start=1
      /protein_id="AAD30633.1"
      /db_xref="GI:4836931"
      /translation="MINPHGGGGEGGEVPKVADFLGVSKSGDHHTDHNLVYPNDIHQT
      NASDYFFQTNSLLPTVVTCASNAPNNYELQESAHNLSLTLSMGSTGAAAAEVATVKA
      SPAETSADNSSSTTNTSGGAIVEATPRRTLETFGQRTSIYRGVTRHRWTGRYEHLWD
      NSCRREGQSRKGRQGGYDKEEKAARAYDLAALKYWGPSTTTNFPITNYEKEVEEMKNM
      TRQEFVASIRRKSSGFSRGASMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEE
      AAEAYDIAAIKFRGLNAVTFEINRYDVKAILESNTLPIGGGAARKLKEAQALESSRK
      REEMIALGSNFHQYGAASGSSSVASSSRLQLQPYPLSIQQPFHLHHHQPLLTQNNN
      DISQYHDSFSYIQTQLHLHQQTNNYLQSSSHTSQLYNAYLQSNPGLLHGFVSDNNNT
      SGFLGNNGIGIGSSSTVGSSAEEEFPAVKVDYDMPPSGGATGYGGWNSGESAQGSNPG
      GVFTMWNE"
gene 38281. .38802
      /gene="F11M15.7"
CDS   38281. .38802
      /gene="F11M15.7"
      /note="Unknown protein; Location of ESTs 136P4T7,
      gb|T45618 and 136P4XP, gb|AA394606"
      /codon_start=1
      /protein_id="AAD30634.1"
      /db_xref="GI:4836932"
      /translation="MDHDKTGCSPPPEGPKLCTNNCGFFGSAATMNMCSKCHKDMLFQ
      QEQGAKFASAVSGTSSSSNIKETFTAALVDIETKSVEPMTVSVQPSVQVVAEVVAP
      EEAAKPKGPSRCTTCNKRVLGTGFKCRGSLFCGTHRYADVHDCSFNYHAAAEQAIK
      ANPVVKAEKLDKI"
gene 40400. .41701

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Query Match 21.8%; Score 91.8; DB 8; Length 105807;
 Best Local Similarity 70.3%; Pred. No. 2.5e-11;
 Matches 137; Conservative 0; Mismatches 57; Indels 1; Gaps 1;

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Qy 222 ggccgaaccggtgcagcgctgcaggaagagggttgacttacgggattcaactgccggt 281
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 38609 GACCAAGCCGATGTACTACTTGCAATAAGCGGGTTGGCCTGACTGGATTCAAATGTCGCT 38668

Qy 282 gtgggaacttgactgcgcactccaccgctactccgacaagcacgactgcaagttcgact 341
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 38669 GTGGGAGCCTCTTCTGCGGAACACACCGCTATGCAGACGTACATGACTGCTCCTTCAATT 38728

Qy 342 aacggactgctgccaaaggacgccattgccaaagggctaataccggtggtgaaggcagacaag 401
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 38729 ACCATGCTGCTGCGCAAGAGGCGATAGCTAA-GGCAAACCCGGTTGTGAAAGCAGAGAAG 38787

Qy 402 ctcgacaagatctaa 416
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Db 38788 CTTGACAAAATCTGA 38802
  
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RESULT 5

AF140722

LOCUS AF140722 844 bp mRNA PLN 07-JUN-2000

DEFINITION Oryza sativa pathogenesis-related protein mRNA, complete cds.

ACCESSION AF140722

VERSION AF140722.1 GI:8307827

KEYWORDS .

SOURCE Oryza sativa.

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 844)

AUTHORS Mukhopadhyay, A. and Tyagi, A.K.

TITLE Isolation and characterization of a novel pathogenesis-related
 protein gene (OSPR) from rice (Oryza sativa cv. Pusa Basmati 1)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 844)

AUTHORS Mukhopadhyay, A. and Tyagi, A.K.

TITLE Direct Submission

JOURNAL Submitted (06-APR-1999) Department of Plant Molecular Biology,
 University of Delhi, South Campus, Benito Juarez Road, New Delhi
 110021, India

FEATURES Location/Qualifiers

source 1..844

/organism="Oryza sativa"

/cultivar="Pusa Basmati 1"

/db_xref="taxon:4530"

CDS 110..604

/note="OSPR"

/codon_start=1

/product="pathogenesis-related protein"

/protein_id="AAF74344.1"

/db_xref="GI:8307828"

/translation="MAQRDKKDQEPTELRAPEITLCANSCGFPGNPATQNLQNCFLA
 ATASTSSPSSLSSPVLDKQPPRPAAPLVEPQAPLPPPVEEMASALATAPAPVAKTSAV"

NRCSRCRKRVGLTGFRRCGHLFCGEHRYSDRHGCSYDYKSAARDAIARDNPVVRAAK
IVRF"

BASE COUNT 206 a 225 c 249 g 164 t
ORIGIN

Query Match 21.5%; Score 90.4; DB 8; Length 844;
Best Local Similarity 64.4%; Pred. No. 1e-10;
Matches 150; Conservative 0; Mismatches 82; Indels 1; Gaps 1;

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Qy 188 ggggtggcgcgatctccaaagggggaaggtanggccgaaccggtgcagcgctgcagg 247
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 377 GCGACGGCGCCGGCGCCGGTTCGCCAAGACGTCGGCGGTGAACCGGTGCTCCAGGTGCCGG 436

Qy 248 aagaggggttgacttacgggattcaactgccggtgtgggaacttgactgcgcactccac 307
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 437 AAGCGTGTCCGGCCTACCGGGTTCCGGTGCCGGTGCGGCCACCTGTTCTGCGGCGAACAC 496

Qy 308 cgctactccgacaagcagcactgcaagttcgactaacggactgctgccaaggacgccatt 367
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 497 CGGTACTCCGACCGCCACGGCTGCAGCTACGACTACAAGTCGGCGGCAAGGGACGCCATC 556

Qy 368 gcccaagggctaataccggtggtgaaggcagacaagctcgacaagatctaagggg 420
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 557 GCC-AGGGACAACCCGGTGGTGCGCGCGGCCAAGATCGTTAGGTTCTGAGAGG 608
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RESULT 6
AC090871/c
LOCUS AC090871 165873 bp DNA HTG 28-JUN-2001
DEFINITION Oryza sativa chromosome 3 clone OSJNBb0060J21, *** SEQUENCING IN
PROGRESS ***, 5 unordered pieces.
ACCESSION AC090871
VERSION AC090871.7 GI:14573697
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 165873)
AUTHORS Buell,R., Hsiao,J., Zismann,V., Moffat,K.M., Hill,J.,
Gansberger,K., Burgess,S., Jarrahi,B., Shvartsbeyn,M., Brenner,M.,
Ciecko,A., Pai,G., Vanaken,S., Hansen,C., Utterbach,T.,
Feldblyum,T., Khalak,H.G., Yuan,Q., Quackenbush,J., White,O.,
Salzberg,S. and Fraser,C.
TITLE Oryza sativa ssp. japonica cv. Nipponbare OSJNBb0060J21 BAC genomic
sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 165873)
AUTHORS Buell,R.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
COMMENT On Jun 28, 2001 this sequence version replaced gi:14333942.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces

| | | | | | | |
Db 87039 TAGGTTCTAAAAGG 87026

RESULT 8

PHVPVPR3A

LOCUS PHVPVPR3A 871 bp mRNA PLN 12-AUG-1994

DEFINITION P.vulgaris PVPR3 protein mRNA, complete cds.

ACCESSION M75856

VERSION M75856.1 GI:169362

KEYWORDS PVPR3 protein.

SOURCE Phaseolus vulgaris cDNA to mRNA.

ORGANISM Phaseolus vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.

REFERENCE 1 (bases 1 to 871)

AUTHORS Sharma,Y.K., Hinojos,C.M. and Mehdy,M.

TITLE cDNA cloning, structure and expression of a novel pathogenesis
related protein in bean

JOURNAL Mol. Plant Microb. Interact. 5, 89-95 (1992)

FEATURES Location/Qualifiers

source 1. .871

/organism="Phaseolus vulgaris"

/db_xref="taxon:3885"

mRNA 1. .871

/gene="PVPR3"

gene 1. .871

/gene="PVPR3"

CDS 116. .529

/gene="PVPR3"

/codon_start=1

/protein_id="AAA33773.1"

/db_xref="GI:169363"

/translation="MAQKAQKNDTDFKVPEPITPCATATAAAATSISEPSRFFDAATP

ATSSRSPPKRSPLLEDAANADRTVASEPKRAVNRCSGCRRRVGLTGFRRCRCDLFCAEH

RYTDRHDCSYDYKTVGREAIARENPVVKA AKIVKV"

primer_bind complement(195. .212)

/gene="PVPR3"

/note="5' primer"

BASE COUNT 209 a 234 c 198 g 230 t

ORIGIN

Query Match 19.4%; Score 81.6; DB 8; Length 871;

Best Local Similarity 63.3%; Pred. No. 1e-08;

Matches 140; Conservative 0; Mismatches 80; Indels 1; Gaps 1;

Qy 196 ggcgatctccaaaggggggaaggtanggccgaaccggtgcagcgctgcaggaagagggt 255

Db 310 GACGGTGGCATCGGAGCCGAAGCGCGCGGTGAACCGGTGCTCGGGATGCCGGCGGCGCGT 369

Qy 256 tggacttacgggattcaactgccggtgtgggaacttgtaactgcgcactccaccgctactc 315

Db 370 CGGGCTGACCGGATTCCGCTGTGCGGTGACCTTTTCTGCGCTGAGCACCGGTACAC 429

Qy 316 cgacaagcacgactgcaagttcgactaacggactgctgccaggacgccattgccaaggg 375
 ||| ||||| | |||| | | | |||| | ||||
 Db 430 GGACCGCCACGACTGCTCCTACGACTACAAGACCGTCGGGAGAGAGGCCATCG-CGAGGG 488

Qy 376 ctaatccggtggtgaaggcagacaagctcgacaagatctaa 416
 |||| | ||||| | ||| || ||| ||| |
 Db 489 AGAATCCCGTCGTGAAGGCCGCGAAGATCGTGAAGGTCTGA 529

RESULT 9

AC090871

LOCUS AC090871 165873 bp DNA HTG 28-JUN-2001

DEFINITION Oryza sativa chromosome 3 clone OSJNBb0060J21, *** SEQUENCING IN
 PROGRESS ***, 5 unordered pieces.

ACCESSION AC090871

VERSION AC090871.7 GI:14573697

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Oryza sativa.

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 165873)

AUTHORS Buell,R., Hsiao,J., Zismann,V., Moffat,K.M., Hill,J.,
 Gansberger,K., Burgess,S., Jarrahi,B., Shvartsbeyn,M., Brenner,M.,
 Ciecko,A., Pai,G., Vanaken,S., Hansen,C., Utterbach,T.,
 Feldblyum,T., Khalak,H.G., Yuan,Q., Quackenbush,J., White,O.,
 Salzberg,S. and Fraser,C.

TITLE Oryza sativa ssp. japonica cv. Nipponbare OSJNBb0060J21 BAC genomic
 sequence

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 165873)

AUTHORS Buell,R.

TITLE Direct Submission

JOURNAL Submitted (13-MAR-2001) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA

COMMENT On Jun 28, 2001 this sequence version replaced gi:14333942.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 11885: contig of 11885 bp in length
 * 11886 11923: gap of unknown length
 * 11924 28536: contig of 16613 bp in length
 * 28537 28574: gap of unknown length
 * 28575 95942: contig of 67368 bp in length
 * 95943 95979: gap of unknown length
 * 95980 122498: contig of 26519 bp in length
 * 122499 122535: gap of unknown length
 * 122536 165873: contig of 43338 bp in length.

FEATURES Location/Qualifiers

source 1. .165873

/organism="Oryza sativa"

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

COMMENT On Aug 9, 2001 this sequence version replaced gi:13486922.
The orientation of the sequence is from T7 to SP6 of the PAC clone.

FEATURES Location/Qualifiers
source 1. .151100
/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="1"
/clone="P0480C01"

BASE COUNT 42198 a 33215 c 33471 g 42216 t
ORIGIN

Query Match 18.6%; Score 78.4; DB 8; Length 151100;
Best Local Similarity 64.4%; Pred. No. 2.7e-08;
Matches 132; Conservative 0; Mismatches 72; Indels 1; Gaps 1;

Qy 212 gggaaggtanggccgaaccggtgcagcgctgcaggaagagggttgacttacgggattc 271
||| | | || | |||| | | || | || | || | || | || | || | || |
Db 108804 GGGGCGAAGACGAAGAGCAGGTGCGCTGCGTGCGGGAGGAGCGTGGGGCTGATGGGGTTC 108863

Qy 272 aactgccggtgtgggaacttgactgcgcactccaccgctactccgacaagcacgactgc 331
| |||| | | | | | || | |||| | | || |||| | || | |||| | || |
Db 108864 GAGTGCCGCTGCGGTGCCGTGTTCTGCGGCGCGCATCGCTACTCGGACAGGCACGACTGC 108923

Qy 332 aagttcgactaacggactgctgccaaggacgccattgccaagggctaataccggtggtgaa 391
| ||| | | | | | | | |||| | || | | | | | | | | |
Db 108924 GGCTACGATTACAGGGGCGCGGGGCGCGACGCCATCGCC-CGCGCCAACCCCGTCGTGAG 108982

Qy 392 ggcagacaagctcgacaagatctaa 416
| |||| | | | | | | |
Db 108983 ACCCGACAAGGTGGAGAAGCTCTGA 109007

RESULT 12
AP003288/c
LOCUS AP003288 159497 bp DNA HTG 21-FEB-2001
DEFINITION Oryza sativa chromosome 1 clone P0683B11, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
ACCESSION AP003288
VERSION AP003288.1 GI:13027318
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Oryza sativa (cultivar:Nipponbare) DNA, clone:P0683B11.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (sites)
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0683B11
JOURNAL Published Only in DataBase (2001) In press
REFERENCE 2 (bases 1 to 159497)
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Direct Submission

```

JOURNAL      Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
              Agrobiological Resources, Rice Genome Research Program; Kannondai
              2-1-2, Tsukuba, Ibaraki 305-8602, Japan
              (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
              Tel:81-298-38-7441, Fax:81-298-38-7468)

COMMENT      NOTE: It currently consists of 1 contigs. Gaps between the contigs
              are represented as runs of N. The order of the pieces is believed
              to be correct as given, however the sizes of the gaps between them
              are based on estimates that have provided by the submitter. This
              sequence will be replaced by the finished sequence as soon as it is
              available and the accession number will be preserved.
              * NOTE: This is a 'working draft' sequence.
              * This sequence will be replaced
              * by the finished sequence as soon as it is available and
              * the accession number will be preserved.

FEATURES
    source          Location/Qualifiers
                    1. .159497
                      /organism="Oryza sativa"
                      /cultivar="Nipponbare"
                      /db_xref="taxon:4530"
                      /chromosome="1"
                      /clone="P0683B11"

BASE COUNT      45304 a  34607 c  35698 g  43688 t      200 others
ORIGIN

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RESULT 13
AY042871
LOCUS      AY042871      871 bp      mRNA      PLN      04-JUL-2001
DEFINITION Arabidopsis thaliana zinc finger-like protein (F3C22_200) mRNA,
            complete cds.
ACCESSION  AY042871
VERSION    AY042871.1  GI:14596166
KEYWORDS   FLI_CDNA.
SOURCE     thale cress.
            ORGANISM  Arabidopsis thaliana

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 871)

AUTHORS Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.

TITLE Direct Submission

JOURNAL Submitted (25-JUN-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

FEATURES Location/Qualifiers

source 1. .871
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /chromosome="III"
 /clone="RAFL04-17-A20"
 /note="This clone is in pBluescript ecotype: Columbia"

gene 1. .871
 /gene="F3C22_200"

CDS 93. .602
 /gene="F3C22_200"
 /codon_start=1
 /product="zinc finger-like protein"
 /protein_id="AAK68811.1"
 /db_xref="GI:14596167"
 /translation="MAEEHRCQTPESNRLCVNCGFLGSATMNLCSNCYGDLCLKQQQ
 QSSSIKSTVESSLVSPSSSSSEISSPIIPLLKNPSVKLEVPEKKAVISLPTTEQN
 QQQRPNRCTTCRKRVLGTGFKCRCGTMFCGVHRYPEIHGCSYDFKSAGREEIAKANPL
 VKAAKLQKI"

BASE COUNT 216 a 208 c 190 g 257 t

ORIGIN

Query Match 17.2%; Score 72.6; DB 8; Length 871;

Best Local Similarity 64.1%; Pred. No. 1.1e-06;
Matches 125; Conservative 0; Mismatches 69; Indels 1; Gaps 1;

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Qy  222 ggccgaaccggtgcagcgcctgcaggaagagggttgacttacgggattcaactgccggt 281
      ||||| ||||| | || ||||| |||| | | || ||||| |||||
Db  409 GGCCGAATCGGTGCACGACGTGTAGGAAACGGGTCGGGTTAACCGGATTCAAGTGCCGGT 468

Qy  282 gtgggaacttgactgcgcactccaccgctactccgacaagcacgactgcaagttcgact 341
      ||| | ||| |||| | || | ||| | || | ||| | ||| |
Db  469 GCGGTACGATGTTTTGCGGGGTTTCATAGGTACCCGGAGATCCATGGATGCAGCTACGATT 528

Qy  342 aacggactgctgccaaaggacgccattgccaaagggttaatccggtggtgaaggcagacaag 401
      | | | | | | | | | | | | | | | | | | | | | |
Db  529 TCAAATCGCCGGACGTGAAGAGATCGCGAA-AGCGAATCCGTTGGTGAAAGCAGCGAAG 587

Qy  402 ctcgacaagatctaa 416
      || | |||| | |
Db  588 CTTCAGAAGATATGA 602

```

RESULT 14

ATF3C22

LOCUS ATF3C22 100028 bp DNA PLN 27-APR-2000

DEFINITION Arabidopsis thaliana DNA chromosome 3, BAC clone F3C22.

ACCESSION AL353912

VERSION AL353912.1 GI:7669934

KEYWORDS .

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 100028)

AUTHORS Purnelle,B., Masuy,D., Goffeau,A., Boutry,M., Mewes,H.W., Rudd,S.,
Lemcke,K., Mayer,K.F.X., Quetier,F. and Salanoubat,M.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 100028)

AUTHORS EU Arabidopsis sequencing,project.

TITLE Direct Submission

JOURNAL Submitted (27-APR-2000) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
Coordinator: Marcel Salanoubat and Francis Quetier, Groupement
d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue
Gaston Cremieux, BP191, 91006 Evry Cedex, France;
<http://www.genoscope.cns.fr>

COMMENT Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

FEATURES Location/Qualifiers

source

1. .100028
/organism="Arabidopsis thaliana"
/variety="Columbia"
/db_xref="taxon:3702"
/chromosome="3"

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1. .31726
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exon      32144. .32312
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RESULT 15

AP002044

LOCUS AP002044 21200 bp DNA PLN 19-JUL-2000

DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MMF12.

ACCESSION AP002044

VERSION AP002044.1 GI:8051652

KEYWORDS .

SOURCE Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1 clone:MMF12.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (sites)

AUTHORS Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.
 TITLE Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC and BAC clones

JOURNAL DNA Res. 7 (3), 217-221 (2000)

MEDLINE 20363099

REFERENCE 2 (bases 1 to 21200)

AUTHORS Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
 TITLE Direct Submission

JOURNAL Submitted (16-MAY-2000) to the DDBJ/EMBL/GenBank databases.
 Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)

COMMENT Address for correspondence: kaos@kazusa.or.jp

For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MMF12
 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/Grail-1.3/>), GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and SplicePredictor (Volker Brendel, Stanford University,

http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
 Genes encoding tRNAs are predicted by tRNAscan-SE
 (Sean Eddy, Washington University School of Medicine, St. Louis,
 http://genome.wustl.edu/eddy/tRNAscan-SE/).
 This sequence may not be the entire insert of this clone. It may be
 shorter because we remove overlaps between neighboring submissions.
 The 5' clone is T16H11 and the 3' clone is MBK21.

FEATURES	Location/Qualifiers
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.12106)

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CDS

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SGLLYIANAGDSRVVLGRLEKAFKIVKAVQLSSEHNASLESVREELRSLHPNDPQIVV
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CDS

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BASE COUNT 6829 a 4011 c 4053 g 6307 t
ORIGIN

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Matches 121; Conservative 0; Mismatches 68; Indels 1; Gaps 1;

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Db 19112 AACCGATGTTCTGGTTGTTCGGAAGAAAGTTGGGTTGACCGGATTGAGGTGCCGATGCGGT 19171
Qy 287 aacttgctactgcgcactccaccgctactccgacaagcacgactgcaagttcgactaacgg 346
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Db 19172 GAGCTTTTCTGCTCAGAGCACCGTTACTCCGATCGTCATGATTGTAGCTACGACTACAAA 19231
Qy 347 actgctgccaaggagcgccattgccaaagggttaatccggtggtgaaggcagacaagctcga 406
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Db 19232 ACCGCTGGTCGTGAGGCGATCG-CTAGAGAAAATCCGGTGGTCAAGGCTGCGAAAATGGT 19290
Qy 407 caagatctaa 416
||| | |||
Db 19291 CAAAGTTTAA 19300

Search completed: February 7, 2002, 11:06:26
Job time: 9912 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2002, 11:00:01 ; Search time 428.31 Seconds
(without alignments)
842.693 Million cell updates/sec

Title: US-09-394-745-6489
Perfect score: 421
Sequence: 1 ggggccagcacgcgtccggc.....ctcgacaagatctaaggggg 421

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
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	2	93	22.1	1116	21	AAC52046	Arabidopsis thalia
	3	91.8	21.8	522	21	AAC43443	Arabidopsis thalia
	4	91.8	21.8	928	21	AAC49898	Arabidopsis thalia
	5	91.8	21.8	986	21	AAC49893	Arabidopsis thalia
	6	81.4	19.3	941	21	AAC40316	Arabidopsis thalia
	7	72.6	17.2	819	21	AAC47807	Arabidopsis thalia
	8	72.6	17.2	896	21	AAC37805	Arabidopsis thalia
	9	72.6	17.2	1155	21	AAC36681	Arabidopsis thalia
	10	71	16.9	1028	21	AAC37406	Arabidopsis thalia
	11	69.2	16.4	830	21	AAC35523	Arabidopsis thalia
	12	68	16.2	348	21	AAC57020	Pinus radiata tran
	13	67	15.9	862	21	AAC40557	Arabidopsis thalia
	14	66.8	15.9	594	21	AAC41669	Arabidopsis thalia
	15	64.4	15.3	1425	22	AAH22181	Human zinc finger
	16	64.4	15.3	2487	21	AAF15969	Human prostate can
	17	62.6	14.9	2517	20	AAZ28269	Rat neuronal immed
	18	61.4	14.6	890	21	AAC47427	Arabidopsis thalia
	19	60.6	14.4	1197	19	AAV61061	Human ubiquitin co
	20	60.6	14.4	1197	20	AAX78444	Human UCSP-2 cDNA.
	21	60.6	14.4	1200	21	AAA39269	cDNA encoding huma
	22	60.6	14.4	1251	22	AAH22180	Human zinc finger
	23	60.6	14.4	1767	22	AAF32722	Human secreted pro
	24	59.6	14.2	855	21	AAC46325	Arabidopsis thalia
	25	59	14.0	1599	22	AAI57828	Human polynucleoti
	26	59	14.0	1637	22	AAI57827	Human polynucleoti
	27	58	13.8	857	21	AAC35304	Arabidopsis thalia
	28	57.4	13.6	831	21	AAC50001	Arabidopsis thalia
	29	57.4	13.6	833	21	AAC49657	Arabidopsis thalia
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	35	54.6	13.0	974	21	AAC34520	Arabidopsis thalia
	36	53.6	12.7	329	21	AAC56980	Pinus radiata tran
	37	48.6	11.5	594	22	AAI41946	Probe #10632 used
	38	45.2	10.7	149	22	AAI54980	Probe #23666 used
	39	44	10.5	378	14	AAQ60725	Human brain Expres
	40	43	10.2	535	22	AAI17609	Probe #7542 for ge
	41	43	10.2	535	22	AAI42527	Probe #11213 used
	42	41.6	9.9	181	21	AAC05414	Human secreted pro
	43	41.6	9.9	183	20	AAX51534	Human secreted pro
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ALIGNMENTS

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 DT 17-OCT-2000 (first entry)
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 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
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 OS Arabidopsis thaliana.
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 PN EP1033405-A2.
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 PD 06-SEP-2000.
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 PF 25-FEB-2000; 2000EP-0301439.
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RESULT 2

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DT 18-OCT-2000 (first entry)

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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 70270.

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KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.
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KW    protein identification; signal transduction pathway;
KW    metabolic pathway; promoter; termination sequence; ss.
XX
OS    Arabidopsis thaliana.
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PN EP1033405-A2.
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DT 18-OCT-2000 (first entry)

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KW metabolic pathway; promoter; termination sequence; ss.

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DT 17-OCT-2000 (first entry)

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KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

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OS Arabidopsis thaliana.

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PN EP1033405-A2.

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PD 06-SEP-2000.

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PF 25-FEB-2000; 2000EP-0301439.

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DT 17-OCT-2000 (first entry)

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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 14694.

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KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

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OS Arabidopsis thaliana.

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PN EP1033405-A2.

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PD 06-SEP-2000.

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PF 25-FEB-2000; 2000EP-0301439.

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PR	04-AUG-1999;	99US-0147204.
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PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
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PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.

PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
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Query Match 17.2%; Score 72.6; DB 21; Length 1155;
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 Db 683 ggccgaatcggtgcacgacgtgtaggaaacgggtcggttaaccggattcaagtgccggt 742

Qy 282 gtgggaacttgactgcgccactccaccgctactccgacaagcacgactgcaagttcgact 341
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 Db 743 gcggtacgatgttttgcgggggttcattaggtaccgagatccatggatgcagctacgatt 802

Qy 342 aacggactgctgccaaaggacgccattgccaaagggttaattccggtggtgaaggcagacaag 401
 | | | | | | | | | | | | | | | | | | | | | |
 Db 803 tcaaatcgccggacgtgaagagatcgcgaa-agcgaatccgttggtgaaagcagcgaag 861

Qy 402 ctcgacaagatctaa 416
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 Db 862 cttcagaagatatga 876

RESULT 10

AAC37406

ID AAC37406 standard; DNA; 1028 BP.

XX

AC AAC37406;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 17264.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

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PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

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PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

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PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

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PR	18-JUN-1999;	99US-0139456.
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PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
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PR	19-JUL-1999;	99US-0144334.
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PR	20-JUL-1999;	99US-0144632.
PR	20-JUL-1999;	99US-0144884.
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PR	21-JUL-1999;	99US-0145086.
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PR	27-JUL-1999;	99US-0145919.
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PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
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PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.

PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
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 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
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 PR 14-OCT-1999; 99US-0159638.
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Query Match 16.9%; Score 71; DB 21; Length 1028;
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 Qy 282 gtgggaacttgactgcgcactccaccgctactccgacaagcacgactgcaagttcgact 341
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 Db 521 tcggtacgatgttttgcgggggttcataaggtaccggagatccatggatgcagctacgatt 580

Qy 342 aacggactgctgccaaggacgccattgccaaagggctaataccggtggtgaaggcagacaag 401
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 Db 581 tcaaatacgccggacgtgaagagatcgcgaa-agcgaatccggtggtgaaagcagcgaag 639

Qy 402 ctcgacaagatctaa 416
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 Db 640 cttcagaagatatga 654

RESULT 11

AAC35523

ID AAC35523 standard; DNA; 830 BP.

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AC AAC35523;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 10502.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

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PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

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PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

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PR 06-MAY-1999; 99US-0132486.

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PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

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PR 14-MAY-1999; 99US-0134221.

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PR	28-MAY-1999;	99US-0136782.
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PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
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PR	05-AUG-1999;	99US-0147192.
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PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
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PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
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PR	26-AUG-1999;	99US-0150884.
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PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
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PR 20-SEP-1999; 99US-0154779.
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 PR 12-OCT-1999; 99US-0158369.
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 PR 14-OCT-1999; 99US-0159329.
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 PR 25-OCT-1999; 99US-0161404.
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 PR 29-OCT-1999; 99US-0162142.

Query Match 16.4%; Score 69.2; DB 21; Length 830;
 Best Local Similarity 63.7%; Pred. No. 1.4e-09;
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 Qy 287 aacttgtagtgcgcactccaccgctactccgacaagcacgactgcaagttcgactaacgg 346
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 Qy 347 actgctgccaaaggacgccattgccaaagggttaataccggtggtgaaggcagacaagctcga 406
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Qy 407 caagatctaa .416
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Db 573 caaagtttaa 582

RESULT 12

AAC57020

ID AAC57020 standard; DNA; 348 BP.

XX

AC AAC57020;

XX

DT 25-JAN-2001 (first entry)

XX

DE Pinus radiata transcription factor DNA sequence #466.

XX

KW Plant; transcription factor; gene expression; eucalyptus; pine; acacia;

KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;

KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;

KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;

KW type 2 Cys2His2; CCAAT box element; MYB; ss.

XX

OS Pinus radiata.

XX

PN WO200053724-A2.

XX

PD 14-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US06112.

XX

PR 11-MAR-1999; 99US-0266513.

PR 18-AUG-1999; 99US-0149485.

XX

PA (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX

PI Wood M, McGrath A, Shenk MA, Glenn M;

XX

DR WPI; 2000-579369/54.

XX

PT New isolated polynucleotide encoding a plant transcription factor for

PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,

PT having modified gene expression or modified activity of a polypeptide

PT -

XX

PS Claim 1; Pages 567-568; 747pp; English.

XX

CC The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding
CC sequence for one such transcription factor. The transcription factor may
CC be used to produce a plant having modified gene expression such as a
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
CC mahogany species or to modify the activity of a polypeptide in a plant.
CC The transcription factors of the present invention are members from the
CC following families of regulatory proteins: bZIP, bZIP family of G-box
CC binding factors, basic helix-loop-helix zipper,
CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2
CC and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements

CC and MYB.
XX
SQ Sequence 348 BP; 81 A; 92 C; 107 G; 68 T; 0 other;

Query Match 16.2%; Score 68; DB 21; Length 348;
Best Local Similarity 63.0%; Pred. No. 2.4e-09;
Matches 104; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

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Qy 267 gattcaactgccggtgtgggaacttgactgcgcactccaccgctactccgacaagcacg 326
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Db 244 gctttaagtgccgctgtggtgaccttttctgcgctcagcacaggtactctgatatgcatg 303

Qy 327 actgcaagttcgactaacggactgctgccaaggacgccattgcc 371
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Db 304 actgctcttttgactacaagactgccggcgctcgccatttctca 348
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RESULT 13

AAC40557

ID AAC40557 standard; DNA; 862 BP.

XX

AC AAC40557;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 28736.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

XX

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

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PR 06-APR-1999; 99US-0128234.

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 PR 10-SEP-1999; 99US-0153070.
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 PR 04-OCT-1999; 99US-0157117.
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 PR 06-OCT-1999; 99US-0157865.
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 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 15.9%; Score 67; DB 21; Length 862;
 Best Local Similarity 62.8%; Pred. No. 5.7e-09;
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Db 476 gatgcttgagctgtaacaagaaagttggcgtgacgggtttcaagtgtaggtgtggaagca 535

Qy 291 tgtactgcgcactccaccgctactccgacaagcagactgcaagttcgactaacggactg 350
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Db 536 ctttctgtggaactcatagatatccagagagtcacgagtgccaattcgatttcaaaggag 595

Qy 351 ctgccaaggacgccattgccaaagggctaatccggtggtgaaggcagacaagctcgacaag 410
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Db 596 ttgcgagagaagctattgctaa-agctaatcctgtggtgaaggctgataaggttgatagg 654

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Db 655 atatgaattgg 665

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RESULT 14

AAC41669

ID AAC41669 standard; DNA; 594 BP.

XX

AC AAC41669;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 32705.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

XX

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

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PR 06-APR-1999; 99US-0128234.

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PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.

PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
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 PR 07-OCT-1999; 99US-0158029.
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 PR 13-OCT-1999; 99US-0159295.
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 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
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 PR 21-OCT-1999; 99US-0160741.
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 PR 21-OCT-1999; 99US-0160768.
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 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
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 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 15.9%; Score 66.8; DB 21; Length 594;
 Best Local Similarity 63.4%; Pred. No. 5.8e-09;
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Qy 351 ctgccaaggacgccattgccaaagggctaatccggtggtgaaggcagacaagctcgacaag 410
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Qy 411 atctaa 416
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 Db 589 atatga 594

RESULT 15

AAH22181

ID AAH22181 standard; cDNA; 1425 BP.

XX

AC AAH22181;

XX

DT 20-AUG-2001 (first entry)

XX

DE Human zinc finger protein (hZNF216) nucleotide sequence.

XX

KW Human; hZNF216-iso; hZNF216; zinc finger protein; ss.

XX

OS Homo sapiens.

XX

PN CN1281898-A.

XX

PD 31-JAN-2001.

XX

PF 27-JUN-2000; 2000CN-0116798.

XX

PR 27-JUN-2000; 2000CN-0116798.

XX

PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.

XX

PI Li N, Xu X, Xiao H;

XX

DR WPI; 2001-282784/30.

DR P-PSDB; AAB98228.

XX

PT New human zinc finger protein isomer, hZNF216, polypeptide and

PT polynucleotide useful for detecting hZNF216 -

XX

PS Example 2; Fig 2; 23pp; Chinese.

XX

CC The present invention describes a human zinc finger protein isomer,
 CC designated hZNF216-iso. Also described are methods for the preparation
 CC and detection of hZNF216-iso protein and nucleotide sequences. The
 CC present sequence represents the human zinc finger protein hZNF216
 CC nucleotide sequence which is given in comparison with the hZNF216-iso
 CC nucleotide sequence in an example from the present invention.

XX

SQ Sequence 1425 BP; 464 A; 279 C; 300 G; 382 T; 0 other;

Query Match 15.3%; Score 64.4; DB 22; Length 1425;
Best Local Similarity 62.1%; Pred. No. 3.3e-08;
Matches 118; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

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Db 492 aacagatgtttcatgtgcagaaagaaagttggtcttacagggttgactgccgatgtgga 551

Qy 287 aacttgactgcgcactccaccgctactccgacaagcacgactgcaagttcgactaacgg 346
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Db 552 aatttgttttgtggacttcaccggttactctgacaagcacaactgtccgtatgattacaaa 611

Qy 347 actgctgccaaggacgccattgccaaagggttaatccggtggtgaaggcagacaagctcga 406
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Db 612 gcagaagctgcag-caaaaatcagaaaagagaatccagttgttggtgaaattca 670

Qy 407 caagatctaa 416
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Db 671 gagaatataa 680
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Search completed: February 7, 2002, 11:00:03
Job time: 4989 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2002, 10:51:52 ; Search time 172.96 Seconds
(without alignments)
551.268 Million cell updates/sec

Title: US-09-394-745-6489
Perfect score: 421
Sequence: 1 ggggccagcacgcgtccggc.....ctcgacaagatctaaggggg 421

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	No.	Score	Match	Length	Match	Length			
	1	60.6	14.4	1197	1	US-08-861-269-4			Sequence 4, Appli
	2	60.6	14.4	1197	2	US-09-134-596-4			Sequence 4, Appli
	3	60.6	14.4	1197	3	US-09-293-273-4			Sequence 4, Appli
c	4	35.8	8.5	7218	1	US-08-232-463-14			Sequence 14, Appli
	5	35.4	8.4	4411529	4	US-09-103-840A-1			Sequence 1, Appli
	6	34.6	8.2	459	2	US-08-387-942C-37			Sequence 37, Appli
	7	34.6	8.2	12588	2	US-08-387-942C-1			Sequence 1, Appli
	8	34.4	8.2	750	3	US-09-167-717-3			Sequence 3, Appli
	9	33.2	7.9	80161	3	US-09-036-987A-1			Sequence 1, Appli
	10	33.2	7.9	80161	4	US-09-370-700-1			Sequence 1, Appli
	11	33.2	7.9	4403765	4	US-09-103-840A-2			Sequence 2, Appli
	12	33	7.8	2899	4	US-08-981-392-24			Sequence 24, Appli
	13	32.4	7.7	4601	1	US-08-470-058-3			Sequence 3, Appli
	14	32.4	7.7	4601	3	US-09-037-188-3			Sequence 3, Appli
	15	32.4	7.7	4601	4	US-09-285-310-3			Sequence 3, Appli
	16	32.4	7.7	5095	1	US-08-092-817-3			Sequence 3, Appli
c	17	32.4	7.7	50937	4	US-09-428-517-1			Sequence 1, Appli
c	18	32.2	7.6	1431	1	US-08-254-357-1			Sequence 1, Appli
c	19	32.2	7.6	4983	1	US-08-472-358-1			Sequence 1, Appli
c	20	32.2	7.6	4983	5	PCT-US92-05786A-1			Sequence 1, Appli
c	21	31.8	7.6	2015	1	US-07-937-609-25			Sequence 25, Appli
c	22	31.8	7.6	2015	4	US-08-029-170-25			Sequence 25, Appli
c	23	31.6	7.5	1950	3	US-08-911-853-14			Sequence 14, Appli
c	24	31.6	7.5	1950	4	US-09-479-409-14			Sequence 14, Appli
	25	31.6	7.5	5247	1	US-08-920-812-15			Sequence 15, Appli
	26	31.6	7.5	5247	1	US-08-920-827-15			Sequence 15, Appli
	27	31.6	7.5	5247	1	US-08-921-177-15			Sequence 15, Appli
	28	31.6	7.5	5247	1	US-08-362-577C-15			Sequence 15, Appli
	29	31.6	7.5	5247	2	US-08-920-828-15			Sequence 15, Appli
	30	31.6	7.5	17612	3	US-08-911-853-29			Sequence 29, Appli
	31	31.6	7.5	17612	4	US-09-479-409-29			Sequence 29, Appli
c	32	31.6	7.5	4403765	4	US-09-103-840A-2			Sequence 2, Appli
c	33	31	7.4	1195	1	US-08-117-373-5			Sequence 5, Appli
c	34	31	7.4	3914	1	US-08-117-373-11			Sequence 11, Appli
	35	31	7.4	11220	4	US-09-105-537-32			Sequence 32, Appli
	36	31	7.4	36778	4	US-09-105-537-5			Sequence 5, Appli
	37	31	7.4	38506	3	US-09-320-878-19			Sequence 19, Appli
c	38	31	7.4	44377	2	US-08-804-227C-7			Sequence 7, Appli
c	39	31	7.4	44377	2	US-08-804-198-1			Sequence 1, Appli
c	40	30.8	7.3	8201	1	US-08-253-155A-9			Sequence 9, Appli
c	41	30.6	7.3	1182	1	US-08-241-943-23			Sequence 23, Appli
c	42	30.6	7.3	2327	6	5229279-5			Patent No. 5229279
c	43	30.6	7.3	2327	6	5512669-5			Patent No. 5512669

c	44	30.6	7.3	4984	1	US-08-687-806-1	Sequence 1, Appli
c	45	30.6	7.3	5392	2	US-08-403-852D-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-08-861-269-4
; Sequence 4, Application US/08861269
; Patent No. 5817494
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: UBIQUITIN CONJUGATION PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,269
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0302 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1197 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT09
; CLONE: 2151473
US-08-861-269-4

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Query Match	14.4%;	Score 60.6;	DB 1;	Length 1197;
Best Local Similarity	60.7%;	Pred. No. 3.8e-08;		

Matches 116; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

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Qy 286 gaacttgctactgcgcactccaccgctactccgacaagcagcactgcaagttcgactaacg 345
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Qy 346 gactgctgccaaaggacgccattgccaaagggttaatccggtggtgaaggcagacaagctcg 405
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Qy 406 acaagatctaa 416
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RESULT 2
US-09-134-596-4
; Sequence 4, Application US/09134596
; Patent No. 5922318
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: UBIQUITIN CONJUGATION PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,596
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/861,269
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0302 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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;   LENGTH: 1197 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: BRAINOT09
;   CLONE: 2151473
US-09-134-596-4

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Query Match          14.4%;   Score 60.6;   DB 2;   Length 1197;
Best Local Similarity 60.7%;   Pred. No. 3.8e-08;
Matches 116;   Conservative 0;   Mismatches 74;   Indels 1;   Gaps 1;

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Qy   286 gaacttggtactgcgcactccaccgctactccgacaagcagcactgcaagttcgactaacg 345
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Qy   346 gactgctgccaaaggacgccattgccaaagggctaataccggtggtgaaggcagacaagctcg 405
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Db   819 AGCCGATGCTGCTGA-GAAAATCAGAAAAGAAAATCCAGTAGTTGTTGGTGAAAAGATCC 877

Qy   406 acaagatctaa 416
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Db   878 AAAAGATTTGA 888

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RESULT 3
US-09-293-273-4
; Sequence 4, Application US/09293273
; Patent No. 6057112
; GENERAL INFORMATION:
;   APPLICANT: Bandman, Olga
;   APPLICANT: Corley, Neil C.
;   APPLICANT: Lal, Preeti
;   APPLICANT: Shah, Purvi
;   TITLE OF INVENTION: UBIQUITIN CONJUGATION PROTEINS
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/293,273
;   FILING DATE:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/134,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0302 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1197 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT09
; CLONE: 2151473
US-09-293-273-4

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Query Match          14.4%; Score 60.6; DB 3; Length 1197;
Best Local Similarity 60.7%; Pred. No. 3.8e-08;
Matches 116; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

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Qy 286 gaacttgactgcgcactccaccgctactccgacaagcacgactgcaagttcgactaacg 345
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Db 819 AGCCGATGCTGCTGA-GAAAATCAGAAAAGAAAATCCAGTAGTTGTTGGTGAAAAGATCC 877

Qy 406 acaagatctaa 416
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Db 878 AAAAGATTTGA 888

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RESULT 4
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria

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; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

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Query Match          8.5%; Score 35.8; DB 1; Length 7218;
Best Local Similarity 1.9%; Pred. No. 0.69;
Matches      7; Conservative 203; Mismatches 156; Indels    0; Gaps    0;

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Qy     116 gtagctgttgcccaagttgagttgcaaacaatgaacgtgcagcagcccgtgatgttgcc 175
      : :: : : :::: :::: : :::: : :::: : :::: : :::: : :::: :
Db    1386 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1327

Qy     176 ggacccagcgaggggggtggcggcgatctccaaaggggggaaggtanggccgaaccggtgc 235
      :::: :: :::: :: :::: :::: :::: :::: :::: :::: :::: ::::
Db    1326 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1267

Qy     236 agcgctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaacttgtag 295
      :: : : :::: :::: : :::: : :::: : :::: : :::: : :::: :
Db    1266 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1207

Qy     296 tgcgcactccaccgctactccgacaagcacgactgcaagttcgactaacggactgctgcc 355

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Db    1206 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1147

Qy     356 aaggacgccattgccaagggctaatccggtggtgaaggcagacaagctcgacaagatcta 415
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    1146 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1087

Qy     416 agggggg 421
      : : : : :
Db    1086 RRRRRR 1081

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Query Match 8.4%; Score 35.4; DB 4; Length 4411529;
Best Local Similarity 48.8%; Pred. No. 8.1;
Matches 123; Conservative 0; Mismatches 127; Indels 2; Gaps 1;

Db 338845 aactgggcatga 338856

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Query Match 8.2%; Score 34.6; DB 2; Length 459;
Best Local Similarity 48.5%; Pred. No. 0.56;
Matches 94; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 171 ttgccggagaccagcgcgaggggtggcgcgcatctccaaagggggaagtanggccgaacc 230
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Db 29 TTTCCGGCAGCAGCGCGGCCGAGGAAC TGCTCGGCGGGGT CGGCAACGACAGCCTGGACG 88

Qy 231 ggtgcagcgcctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaact 290
 | | | | | | | | | | | | | | | | | | | | |
 Db 89 GCGGCGCCGGCAACGACATCCTCGACGGCGGGGCGGGGCGCGACACCCTGAGTGGCGGCA 148

Qy 291 tgtactgcgcactccaccgctactccgacaagcacgactgcaagttcgactaacggactg 350
 | | | | | | | | | | | | | | | | | | | | |
 Db 149 GCGGCGAGCGACATCTTCCGCTTCGGCGGCGCGCTCGACAGCTTCGCAACTACGCCAGCG 208

Qy 351 ctgccaaggacgcc 364
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 Db 209 GGACGAACGGCACC 222

RESULT 7

US-08-387-942C-1

; Sequence 1, Application US/08387942C

; Patent No. 5939289

; GENERAL INFORMATION:

; APPLICANT: ERTESVAG, HELGA

; APPLICANT: VALLA, SVEIN

; APPLICANT: SKJAK-BRAEK, GUDMUND

; APPLICANT: LARSEN, BJORN

; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES

; TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP

; STREET: P.O.BOX 747

; CITY: FALLS CHURCH

; STATE: VA

; COUNTRY: USA

; ZIP: 22042

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/387,942C

; FILING DATE: 09-MAY-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MURPHY JR, GERALD M.

; REGISTRATION NUMBER: 28,977

; REFERENCE/DOCKET NUMBER: 1809-106P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-205-8000

; TELEFAX: 703-205-8050

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12588 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; ORGANISM: Azotobacter vinelandii

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; STRAIN: E
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 290..1951
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2227..6438
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6702..9695
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9973..12588
US-08-387-942C-1

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Query Match 8.2%; Score 34.6; DB 2; Length 12588;
Best Local Similarity 48.5%; Pred. No. 1.8;
Matches 94; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy	171	ttgccggaccacagcagaggggtggcggcgatctccaaaggggggaaggtanggccgaacc	230
Db	9205	TTTCCGGCAGCAGCGCGGCCGAGGAAGTCTCGGCGGGGTCGGCAACGACAGCCTGGACG	9264
Qy	231	ggtgcagcgcctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaact	290
Db	9265	GCGGCGCCGGCAACGACATCCTCGACGGCGGGGCGGGGCGCGACACCTGAGTGGCGGCA	9324
Qy	291	tgtactgcgcaactccaccgctactccgacaagcacgactgcaagttcgactaacggactg	350
Db	9325	GCGGCAGCGACATCTTCCGCTTCGGCGGCGCGCTCGACAGCTTCCGCAACTACGCCAGCG	9384
Qy	351	ctgccaaaggacgcc	364
Db	9385	GGACGAACGGCACC	9398

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RESULT      8
US-09-167-717-3
; Sequence 3, Application US/09167717
; Patent No. 6133014
; GENERAL INFORMATION:
; APPLICANT: MUKOUYAMA, MASAHARU
; APPLICANT: YASUDA, SHINZO
; APPLICANT: KOMATSUZAKI, SATOMI
; TITLE OF INVENTION: MALEATE ISOMERASE GENE
; FILE REFERENCE: PH-555US
; CURRENT APPLICATION NUMBER: US/09/167,717
; CURRENT FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: JP 276261/1997
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 3
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Pseudomonas fluorescens
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (1)..(750)
US-09-167-717-3

Query Match 8.2%; Score 34.4; DB 3; Length 750;
Best Local Similarity 48.9%; Pred. No. 0.76;
Matches 92; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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Qy      14  gtccggcaggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagc 73
          | ||| || || || || || || || || || || || || || || || ||
Db      511  gcccggtcacgacacggccaacctgccgggcatcgcgccggcatgaaccttgagggcgctc 570

Qy      74  gacgccgtcatggagccggttggtgctggcagcaacacggtagtagctggtgccaagtt 133
          || | || || || || || || || || || || || || || || || ||
Db      571  gatgtggtggtgctttcagcctgcgtgcagatgcagtcgctgccggcagtcgccaaggtc 630

Qy     134  gagttgcaaacaatgaacgtgcagcagcccgcgtgatggtgccggaccagcgagggggtg 193
          ||| || || || || || || || || || || || || || || || ||
Db     631  gaggcgcaaaccggcaaaccggtggtcaccgctgccatgccaccacctacgccatgctc 690

Qy     194  gcggcgat 201
          |||| |
Db     691  aaggcgct 698
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RESULT 9

US-09-036-987A-1

; Sequence 1, Application US/09036987A

; Patent No. 6143526

; GENERAL INFORMATION:

; APPLICANT: Baltz, Richard H.

; APPLICANT: Broughton, Mary C.

; APPLICANT: Crawford, Kathryn P.

; APPLICANT: Madduri, Krishnamurthy

; APPLICANT: Merlo, Donald J.

; APPLICANT: Treadway, Patti J.

; APPLICANT: Turner, Jan R.

; APPLICANT: Waldron, Clive

; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide

; TITLE OF INVENTION: Production

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dow AgroSciences LLC Patent Department

; STREET: 9330 Zionsville Road

; CITY: Indianapolis

; STATE: Indiana

; COUNTRY: USA

; ZIP: 46268

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/036,987A

; FILING DATE: 09-MAR-1998

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; REGISTRATION NUMBER: 28,479
; REFERENCE/DOCKET NUMBER: 50,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80161 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-036-987A-1

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Query Match          7.9%; Score 33.2; DB 3; Length 80161;
Best Local Similarity 55.1%; Pred. No. 8.8;
Matches 65; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy      23 gatcaggccaagctggctgcctcctctatcgacagcatcgtaacggcagcgacgccgtc 82
        ||||| | | | | | | | | | | | | | | | | | | |
Db 21852 GATCAGGCGCACGCCGATGGCGACCGGATCTACTGCCTCATCCGCGGCAGCGCGGTCAAC 21911

Qy      83 atggagccggttggttgctggcagcaacacggtagtagctggtgcccagttgagttgc 140
        | || | | | | | | | | | | | | | | | | |
Db 21912 AACGATGGGGGCGGTGCCGGGCTACCGTTCCGGCGGCGGACGCCAGGCGGAGCTGC 21969

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RESULT 10
US-09-370-700-1
; Sequence 1, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/370,700
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 80161
; TYPE: DNA
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-1

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Query Match 7.9%; Score 33.2; DB 4; Length 80161;
Best Local Similarity 55.1%; Pred. No. 8.8;
Matches 65; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy      23 gatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgccgtc 82
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Db 21852 gatcaggcgcacgccgatggcgaccggatctactgcctcatccgcggcagcgcggtcaac 21911

Qy      83 atggagccggttggttgctggcagcaacacggtagtagctggtgccaagttgagttgc 140
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Db 21912 aacgatggggggcggtgccgggtcaccgttcggcgggcgagcggagcggagctgc 21969
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RESULT 11
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 7.9%; Score 33.2; DB 4; Length 4403765;
Best Local Similarity 47.0%; Pred. No. 26;
Matches 102; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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Qy      179 cccagcgaggggggtggcgcgatctccaaaggggggaaggtanggccgaaccggtgcagc 238
      ||| |||| | | | |||| | | | | | | | | | |
Db 1383125 ccccgcgagcggttctcgcgctcaccgggtggaccacaatcggcgatctcgagctg 1383184

Qy      239 gcctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaacttgactgc 298
      ||| || | | | | | | | | | | | | | | |
Db 1383185 gccgccaagaccggcgcgcggtcaccgacatcaagaagatgacgatctggggcaatcac 1383244

Qy      299 gcactccaccgctactccgacaagcacgactgcaagttcgactaacggactgctgccaag 358
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Db 1383245 tcggccaccagtagcccgacctgttcacgcggaggtcgccggaaagaacgcggccgaa 1383304
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Qy 359 gacgccattgcccaagggctaataccggtggtgaaggca 395
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RESULT 12
US-08-981-392-24
; Sequence 24, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; 'ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2899 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-981-392-24

Query Match 7.8%; Score 33; DB 4; Length 2899;
Best Local Similarity 35.3%; Pred. No. 3;
Matches 78; Conservative 31; Mismatches 112; Indels 0; Gaps 0;

Qy 147 tgaacgtgcagcagcccgctgatgttgccggacccagcagagggggtggcggcgatctcca 206

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      |||: |:||| |:| | : :|:| :||| | : |||:| | |:| :| | |
Db   1750 TGARGCTRCAGAARCAACCRGCCYCCASCYGAMCCCTGNSGGGGRGAGACRGARACCATGA 1809

Qy   207 aaggggggaaggtangggccgaaccggtgcagcgcctgcaggaagaggggttgacttacgg 266
      | : | | | : | | : | | | :||| :||:
Db   1810 ACAACCTRGNCAAYTGCCAGCGYGAGAAGGACRTYTCWGTYAGCATCATYGGGGNYACSC 1869

Qy   267 gattcaactgccggtgtggaacttgactgcgcactccaccgctactccgacaagcacg 326
      |||| | || | ||| : ||| : ||:|:|||| ::
Db   1870 ACATCAAGAACACCAACAAGAAGGCGGACTTYCACGGGGACCAYRGNGCCRASAAAGARYR 1929

Qy   327 actgcaagttcgactaacggactgctgccaaggacgccatt 367
      || :||| :| :|| | : :| | | | || | |:
Db   1930 GCTTYAAGGYCCGMTACCCMRNKGTGGACTATAACCTCGTK 1970

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RESULT 13

US-08-470-058-3

; Sequence 3, Application US/08470058

; Patent No. 5817789

; GENERAL INFORMATION:

; APPLICANT: Heartlein, Michael W.

; APPLICANT: Lemontt, Jeffrey F.

; TITLE OF INVENTION: Chimeric Proteins For Use in Transport

; TITLE OF INVENTION: of a Selected Substance Into Cells

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: MA

; COUNTRY: USA

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,058

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 32,227

; REFERENCE/DOCKET NUMBER: TKT93-01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4601 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: both

; MOLECULE TYPE: cDNA to mRNA

US-08-470-058-3

Query Match 7.7%; Score 32.4; DB 1; Length 4601;
Best Local Similarity 58.2%; Pred. No. 5.3;
Matches 57; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy      20 caggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgcc 79
          |||| | | | ||||| || || ||||| | | || | |||| |
Db      1433 CAGGCCCCCGACGGGCTGGCTGTGGACTGGATCCACAGCAACATCTACTGGACCGACTCT 1492

Qy      80 gtcattggagccggttggtgctggcagcaacacggtagt 117
          ||| ||| | || || || | || || ||
Db      1493 GTCCTGGGCACTGTCTCTGTTGCGGATACCAAGGGCGT 1530
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RESULT 14

US-09-037-188-3

; Sequence 3, Application US/09037188

; Patent No. 6027921

; GENERAL INFORMATION:

; APPLICANT: Heartlein, Michael W.

; APPLICANT: Lemontt, Jeffrey F.

; APPLICANT: Concino, Michael F.

; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE

; TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/037,188

; FILING DATE: 02-MAR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Fraser, Ph.D., J.D., Janis K.

; REGISTRATION NUMBER: 34,819

; REFERENCE/DOCKET NUMBER: 07236/009002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4601 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: both
; MOLECULE TYPE: cDNA to mRNA
US-09-037-188-3

Query Match 7.7%; Score 32.4; DB 3; Length 4601;
Best Local Similarity 58.2%; Pred. No. 5.3;
Matches 57; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 20 caggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgagcc 79
|||| | | | ||||| || || ||||| | | || | |||||
Db 1433 CAGGCCCCCGACGGGCTGGCTGTGGACTGGATCCACAGCAACATCTACTGGACCGACTCT 1492

Qy 80 gtcattggagccggttggtgctggcagcaacacggtagt 117
||| ||| | || || || | || || ||
Db 1493 GTCCTGGGCACTGTCTCTGTTGCGGATACCAAGGGCGT 1530

RESULT 15
US-09-285-310-3

; Sequence 3, Application US/09285310
; Patent No. 6262026
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemontt, Jeffrey F.
; APPLICANT: Concino, Michael F.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
; TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,310
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/037,188
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 07236/009002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 4601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA to mRNA
US-09-285-310-3

Query Match 7.7%; Score 32.4; DB 4; Length 4601;
Best Local Similarity 58.2%; Pred. No. 5.3;
Matches 57; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 20 caggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgcc 79
|||| | | | ||||| || ||| ||||| | | || | |||||
Db 1433 CAGGCCCCGACGGGCTGGCTGTGGACTGGATCCACAGCAACATCTACTGGACCGACTCT 1492

Qy 80 gtcattggagccggttgctggcagcaacacggtagt 117
||| ||| | || || || | || || ||
Db 1493 GTCCTGGGCACTGTCTCTGTTGCGGATACCAAGGGCGT 1530

Search completed: February 7, 2002, 11:12:10
Job time: 7296 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2002, 08:20:48 ; Search time 4942.22 Seconds
(without alignments)
915.373 Million cell updates/sec

Title: US-09-394-745-6489
Perfect score: 421
Sequence: 1 ggggccagcacgcgtccggc.....ctcgacaagatctaaggggg 421

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*

4: em_estom:*
 5: em_estpl:*
 6: em_estba:*
 7: em_estro:*
 8: em_estov:*
 9: em_htc:*
 10: gb_est1:*
 11: gb_est2:*
 12: gb_htc:*
 13: gb_gss:*
 14: em_gss_fun:*
 15: em_gss_hum:*
 16: em_gss_inv:*
 17: em_gss_pln:*
 18: em_gss_pro:*
 19: em_gss_rod:*
 20: em_gss_vrt:*
 21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
c	1	385.2	91.5	635	11	BG841717		BG841717	MEST24-E1
	2	378.8	90.0	528	10	BE012241		BE012241	945015H01
c	3	378.8	90.0	629	10	AW506899		AW506899	660060H09
	4	367.4	87.3	602	10	AW928018		AW928018	945006F08
	5	362.2	86.0	477	10	BE640589		BE640589	945020B04
	6	351.8	83.6	518	10	BE129631		BE129631	945027C01
	7	348.8	82.9	594	10	AI881804		AI881804	606073E02
	8	331.4	78.7	488	11	BG355155		BG355155	947043D10
c	9	324.8	77.1	482	10	BE510926		BE510926	946056E05
	10	312.8	74.3	567	10	AW927909		AW927909	945010H04
c	11	290.6	69.0	643	10	AI977903		AI977903	496035D05
c	12	290	68.9	514	10	AW061851		AW061851	687007F12
	13	287.4	68.3	527	10	AI649645		AI649645	486077B07
c	14	276.8	65.7	599	10	BE129734		BE129734	946003G07
	15	264.2	62.8	660	11	W99253		W99253	EST01 Gluco
	16	263.8	62.7	598	10	AW924551		AW924551	WS1_70_F0
	17	260.6	61.9	582	10	BE361054		BE361054	DG1_69_E0
	18	259.6	61.7	595	11	BI246082		BI246082	IP1_68_E1
	19	259.4	61.6	479	11	BE918267		BE918267	OV1_1_C02
	20	258	61.3	549	10	AW231809		AW231809	687042A08
	21	256.6	61.0	547	11	BE918046		BE918046	OV1_1_C02
	22	255.4	60.7	586	10	BE363253		BE363253	WS1_61_F0
c	23	254.4	60.4	608	10	BE055927		BE055927	945020B03
c	24	254.2	60.4	612	10	AI734759		AI734759	606036A08
	25	253.4	60.2	662	11	BG932962		BG932962	DG1_69_E0
c	26	247.2	58.7	594	10	AI622011		AI622011	486031B05
c	27	245	58.2	651	10	AI861117		AI861117	603012D01
	28	244	58.0	555	10	AW680999		AW680999	WS1_9_D08
	29	243.6	57.9	662	11	BG464005		BG464005	EM1_52_E0

	30	241.6	57.4	649	11	BG465281	BG465281	EM1_74_C1
c	31	241.4	57.3	582	10	AI691879	AI691879	606011G11
c	32	238	56.5	327	10	AW433452	AW433452	707069H08
	33	234.8	55.8	491	10	AW924565	AW924565	WS1_70_F0
	34	232.4	55.2	473	10	BE051771	BE051771	za87h06.g
c	35	230.6	54.8	467	10	AI861162	AI861162	603017B08
	36	221	52.5	231	10	BE640588	BE640588	945020B03
	37	219	52.0	538	11	BG313898	BG313898	WHE2066_D
	38	217	51.5	525	11	BG356205	BG356205	EM1_22_G0
	39	216.2	51.4	620	11	BF473074	BF473074	WHE0925_D
	40	216.2	51.4	693	10	BE585592	BE585592	EST#5PSP6
	41	215	51.1	571	10	BE420025	BE420025	WWS02.C8R
	42	213.6	50.7	260	10	BE056027	BE056027	945017E04
c	43	211.6	50.3	830	10	BE705552	BE705552	Sc01_03a0
	44	211	50.1	664	10	BE431005	BE431005	SUN010.CO
c	45	210.8	50.1	715	10	BE705540	BE705540	Sc01_02h0

ALIGNMENTS

RESULT 1
BG841717/c
LOCUS BG841717 635 bp mRNA EST 29-MAY-2001
DEFINITION MEST24-E10.T3 ISUM4-TN Zea mays cDNA clone MEST24-E10 3', mRNA sequence.
ACCESSION BG841717
VERSION BG841717.2 GI:14244031
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 635)
AUTHORS Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S.
TITLE Expressed Sequence Tags from B73 Maize Seedlings and Silks
JOURNAL Unpublished (2001)
COMMENT On May 25, 2001 this sequence version replaced gi:14208039.
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
PCR Primers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
FEATURES
source Location/Qualifiers
1. .635
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST24-E10"
/clone_lib="ISUM4-TN"

/tissue_type="Seedling and silk"
/lab_host="DH10B"
/note="Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5'
AACTGGAAGAATTCGCGGCCGAGGAATTTTTTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT7T3PAC vector. The library
then went through one round of normalization to CoT value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

BASE COUNT 132 a 190 c 166 g 147 t
ORIGIN

Query Match 91.5%; Score 385.2; DB 11; Length 635;
Best Local Similarity 98.8%; Pred. No. 4e-82;
Matches 398; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy      19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgatgaacggcagcgacgc 78
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Db      630 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 571

Qy      79 cgtcatggagccggttggtgctggcagcaacacggtagtagctggtgccaagttgagtt 138
      |||
Db      570 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTTGAGTT 511

Qy     139 gcaaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgagggggtggcggc 198
      |||
Db      510 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 451

Qy     199 gatctccaaaggggggaaggtanggccgaaccggtgcagcgcctgcaggaagaggggttg 258
      |||
Db      450 GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 391

Qy     259 acttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccga 318
      |||
Db      390 ACTTACGGGATTCAACTGCCGGTGTGGGAAGTTGTACTGCGCACTCCACCGCTACTCCGA 331

Qy     319 caagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaaagggcta 378
      |||
Db      330 CAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA-GGCTA 272

Qy     379 atccggtggtgaaggcagacaagctcgacaagatctaaggggg 421
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Db      271 ATCCGGTGGTGAAGGCAGACAAGCTCGACAAGATCTAGGGGGG 229

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RESULT 2
BE012241
LOCUS BE012241 528 bp mRNA EST 06-JUN-2000
DEFINITION 945015H01.Y1 945 - Mixed adult tissues from Walbot lab, same as 707

(SK) Zea mays cDNA, mRNA sequence.

ACCESSION BE012241

VERSION BE012241.1 GI:8273149

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 528)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945015 row: H column: 01.

FEATURES Location/Qualifiers

source 1..528
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
/note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."

BASE COUNT 120 a 146 c 176 g 86 t

ORIGIN

Query Match 90.0%; Score 378.8; DB 10; Length 528;
Best Local Similarity 97.8%; Pred. No. 1.3e-80;
Matches 394; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgatgaacggcagcgacgc 78
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Db 127 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 186

Qy 79 cgtcatggagccggttgctggcagcaacacggtagtagctggtgcccagttgagtt 138
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Db 187 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTCGAGTT 246

Qy 139 gcaaacaatgaacgtgcagcagcccgctgatggttgccggaaccagcgaggggggtggcggc 198
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Db 247 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGAACCCAGCGAGGGGGTGGCGGC 306

Qy 199 gatctccaaaggggggaaggtanggccgaaccggtgcagcgctgcaggaagagggttg 258
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 Db 307 GATCTCCAAAGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 366
 Qy 259 acttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccga 318
 ||
 Db 367 GCTCACGGGATTCAACTGCCGGTGTGGGAAGTTGTACTGCGCGCTCCACCGCTACTCCGA 426
 Qy 319 caagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaaagggtta 378
 |||
 Db 427 CAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA-GGCTA 485
 Qy 379 atccggtggtgaaggcagacaagctcgacaagatctaaggggg 421
 |||
 Db 486 ATCCGGTGGTGAAGGCAGACAAGCTCGACAAGATCTAGGGGGG 528

RESULT 3
 AW506899/c
 LOCUS AW506899 629 bp mRNA EST 03-MAR-2000
 DEFINITION 660060H09.x1 660 - Mixed stages of anther and pollen Zea mays cDNA,
 mRNA sequence.
 ACCESSION AW506899
 VERSION AW506899.1 GI:7145418
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 629)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 660060 row: H column: 09.
 FEATURES Location/Qualifiers
 source 1. .629
 /organism="Zea mays"
 /cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_lib="660 - Mixed stages of anther and pollen"
 /tissue_type="whole premieotic anthers to pollen shed"
 /dev_stage="premieotic anthers to pollen shed"
 /lab_host="XL0LR"
 /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
 Site_2: XhoI; Anther and pollen cDNA library.
 Directionally sequenced with 5' end at the EcoRI site.
 Created by Amie Franklin."

BASE COUNT 137 a 193 c 171 g 128 t
ORIGIN

Query Match 90.0%; Score 378.8; DB 10; Length 629;
Best Local Similarity 97.8%; Pred. No. 1.4e-80;
Matches 394; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

```
Qy     19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgc 78
      |||
Db    622 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 563

Qy     79 cgtcatggagccggttggttgctggcagcaacacggtagtagctggtgcccagttgagtt 138
      |||
Db    562 CGTCATGGAGCCGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTCGAGTT 503

Qy    139 gcaaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggtggcggc 198
      |||
Db    502 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 443

Qy    199 gatctccaaaggggggaaggtangggccgaaccgggtgcagcgccctgcaggaagaggggttg 258
      |||
Db    442 GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 383

Qy    259 acttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccga 318
      ||
Db    382 GCTCACGGGATTCAACTGCCGGTGTGGGAAGTTGTACTGCGCGCTCCACCGCTACTCCGA 323

Qy    319 caagcacgactgcaagttcgactaacggactgctgccaaaggacgccattgccaaagggcta 378
      |||
Db    322 CAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA-GGCTA 264

Qy    379 atccggtggtgaaggcagacaagctcgacaagatctaaggggg 421
      |||
Db    263 ATCCGGTGGTGAAGGCAGACAAGCTCGACAAGATCTAGGGGGG 221
```

RESULT 4

AW928018

LOCUS AW928018 602 bp mRNA EST 30-MAY-2000

DEFINITION 945006F08.Y1 945 - Mixed adult tissues from Walbot lab, same as 707
(SK) Zea mays cDNA, mRNA sequence.

ACCESSION AW928018

VERSION AW928018.1 GI:8103377

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 602)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
Department of Biological Sciences

Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 945006 row: F column: 08.

FEATURES Location/Qualifiers
 source 1. .602
 /organism="Zea mays"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /clone_lib="945 - Mixed adult tissues from Walbot lab,
 same as 707 (SK)"
 /tissue_type="tassel, kernal, silk, husk, root, leaf"
 /dev_stage="fully-grown"
 /lab_host="DH10B"
 /note="Organ: tassel, kernal, silk, husk, root, leaf;
 Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
 differentiated maize tissues from an active Mutator plant.
 Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
 root, leaf). Unidirectionally cloned. New library number
 given to library 707 for additional sequencing."
 BASE COUNT 134 a 176 c 191 g 101 t
 ORIGIN

Query Match 87.3%; Score 367.4; DB:10; Length 602;
 Best Local Similarity 97.9%; Pred. No. 7e-78;
 Matches 382; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

```

Qy      19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgc 78
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 273

Qy      79 cgtcatggagccggttggttgctggcagcaacacggtagtagctggtgcccaggttgagtt 138
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTCGAGTT 333

Qy      139 gcaaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggtggcggc 198
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 393

Qy      199 gatctccaaaggggggaaggtanggccgaaccggtgcagcgcctgcaggaagaggggttg 258
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 453

Qy      259 acttacgggattcaactgccggtgtgggaacttgtaactgcgcactccaccgctactccga 318
         || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 GCTCACGGGATTCAACTGCCGGTGTGGGAACCTGTACTGCGCGCTCCACCGCTACTCCGA 513

Qy      319 caagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaaagggcta 378
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 CAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA-GGCTA 572

Qy      379 atccggtggtgaaggcagacaagctcgaca 408
         |||||||||||||||||||||||||||||||
Db      573 ATCCGGTGGTGAAGGCAGACAAGCTCGACA 602
  
```

RESULT 5
 BE640589
 LOCUS BE640589 477 bp mRNA EST 30-AUG-2000
 DEFINITION 945020B04.X1 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence..
 ACCESSION BE640589
 VERSION BE640589.1 GI:9954021
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 477)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 945020 row: B column: 04.
 FEATURES Location/Qualifiers
 source 1. .477
 /organism="Zea mays"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
 /tissue_type="tassel, kernal, silk, husk, root, leaf"
 /dev_stage="fully-grown"
 /lab_host="DH10B"
 /note="Organ: tassel, kernal, silk, husk, root, leaf; Vector: pGAD10; Site_1: EcoRI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
 BASE COUNT 109 a 130 c 151 g 87 t
 ORIGIN

Query Match 86.0%; Score 362.2; DB 10; Length 477;
 Best Local Similarity 96.2%; Pred. No. 1.2e-76;
 Matches 381; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

Qy 19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgatgaacggcagcgacgc 78
 |||||||||||||||||||||||||||||||||||||||||
 Db 83 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAATCTTTTCGACGC 142
 Qy 79 cgtcatggagccggttggttgctggcagcaacacggtagtagctggtgcccagttgagtt 138

```

      |||
Db    143 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGGTGCCCAAGTCGAGTT 202
      |||
Qy    139 gcaaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggtggcggc 198
      |||
Db    203 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 262
      |||
Qy    199 gatctccaaaggggggaaggtangggccgaaccggtgcagcgcctgcaggaagaggggttg 258
      |||
Db    263 GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 322
      |||
Qy    259 acttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccga 318
      |||
Db    323 GCTCACGGGATTCAACTGCCGGTGTGGGAAGTTGTACTGCGCGCTCCACCGCTACTCCGA 382
      |||
Qy    319 caagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaaagggcta 378
      |||
Db    383 CAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA-GGCTA 441
      |||
Qy    379 atccggtggtgaaggcagacaagctcgacaagatct 414
      |||
Db    442 ATCCGGTGGTGAAGGCAGACAAGCTCGACAAGATCT 477

```

RESULT 6

BE129631

LOCUS BE129631 518 bp mRNA EST 21-JUN-2000

DEFINITION 945027C01.X2 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.

ACCESSION BE129631

VERSION BE129631.1 GI:8576994

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 518)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945027 row: C column: 01.

FEATURES

source

Location/Qualifiers

1. .518

/organism="Zea mays"

/cultivar="W23"

/db_xref="taxon:4577"

/clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"

```

/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
/note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."

```

```

BASE COUNT      105 a      141 c      169 g      103 t
ORIGIN

```

```

Query Match          83.6%;  Score 351.8;  DB 10;  Length 518;
Best Local Similarity 97.6%;  Pred. No. 3.6e-74;
Matches 367;  Conservative 0;  Mismatches 8;  Indels 1;  Gaps 1;

```

```

Qy      46 ctctatcgacagcatcgtgaacggcagcgacgccgtcatggagccggttggtgctggcag 105
      |||
Db       1 CTCTATCGACAGCATCGTGAACGGCAGCGACGCCGTCATGGAGCCGTTGTTGCTGGCAG 60

Qy     106 caacacggtagtagctggttgcccaagttgagttgcaaacaatgaacgtgcagcagcccg 165
      |||
Db      61 CAACACGGTAGTAGCTGTTGCCCAAGTCGAGTTGCAAACAATGAACGTGCAGCAGCCCGC 120

Qy     166 tgatggttgccggacccagcgaggggggtggcgcgatctccaaaggggggaaggtangggcc 225
      |||
Db     121 TGATGTTGCCGGACCCAGCGAGGGGGTGGCGGCGATCTCCAAAGGGGGGAAGGTAGGGCC 180

Qy     226 gaaccggtgcagcgccctgcaggaagaggggttgacttacgggattcaactgccggtgtgg 285
      |||
Db     181 GAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGGGCTCACGGGATTCAACTGCCGGTGTGG 240

Qy     286 gaacttgtagctgcgcactccaccgctactccgacaagcagcactgcaagttcgactaacg 345
      |||
Db     241 GAACTTGTACTGCGCGCTCCACCGCTACTCCGACAAGCACGACTGCAAGTTGCGACTACCG 300

Qy     346 gactgctgccaaaggacgccattgccaaagggctaataccggtggtgaaggcagacaagctcg 405
      |||
Db     301 GACTGCTGCCAGGGACGCCATTGCCAA-GGCTAATCCGGTGGTGAAGGCAGACAAGCTCG 359

Qy     406 acaagatctaaggggg 421
      |||
Db     360 ACAAGATCTAGGGGGG 375

```

```

RESULT 7
AI881804
LOCUS      AI881804      594 bp      mRNA      EST      02-FEB-2000
DEFINITION 606073E02.y1 606 - Ear tissue cDNA library from Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION  AI881804
VERSION    AI881804.1  GI:5566893
KEYWORDS   EST.
SOURCE     Zea mays.
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 594)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 606073 row: E column: 02.

FEATURES Location/Qualifiers

source 1. .594
 /organism="Zea mays"
 /cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_lib="606 - Ear tissue cDNA library from Schmidt
 lab"
 /tissue_type="mixed"
 /dev_stage="ear length from 0.5 cm - 2.0 cm"
 /lab_host="XL0LR (Stratagene)"
 /note="Organ: immature ear; Vector: pBK-CMV; Site_1: EcoRI
 ; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt
 lab"

BASE COUNT 132 a 173 c 191 g 98 t

ORIGIN

Query Match 82.9%; Score 348.8; DB 10; Length 594;
 Best Local Similarity 95.2%; Pred. No. 1.9e-73;
 Matches 359; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgatgaacggcagcgacgc 78
 |||

Db 215 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 274

Qy 79 cgtcatggagccggttggttgctggcagcaacacggtagtagctggtgccccagttgagtt 138
 |||

Db 275 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTCGAGTT 334

Qy 139 gcaaacaatgaacgtgcagcagcccgctgatggtgcccggacccagcgaggggggtggcggc 198
 |||

Db 335 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 394

Qy 199 gatctccaaaggggggaaggtanggccgaaccggtgcagcgccctgcaggaagaggggttg 258
 |||

Db 395 GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 454

Qy 259 acttacgggattcaactgccggtgtgggaacttgtagtgcgcactccaccgctactccga 318
 ||

Db 455 GCTCACGGGATTCAACTGCCGGTGTGGGAAGTTGTACTGCGCGCTCCACCGCTACTCCGA 514

Qy 319 caagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaagggcta 378

```

      |||
Db    515 CAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAAGGCTAA 574
      |||
Qy    379 atccggtggtgaaggca 395
      |||
Db    575 TCCGGGGGAAGCAGACA 591

```

RESULT 8

BG355155

LOCUS	BG355155	488 bp	mRNA	EST	06-MAR-2001
-------	----------	--------	------	-----	-------------

DEFINITION 947043D10.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA sequence.

ACCESSION BG355155

VERSION BG355155.1 GI:13237141

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM *Zea mays*

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 488)

AUTHORS Walbot, V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V

Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 947043 row: D column: 10.

FEATURES

source

Location/Qualifiers

1. .488

```
/organism="Zea mays"
```

/cultivar="B73"

```
/db xref="taxon:4577"
```

```
/clone lib="947 - 2 week shoot from Barkan lab"
```

```
/tissue type="leaf and stem, including leaf base"
```

```
/dev stage="2 week old seedling (3 leaves)"
```

```
/lab host="XL1-Blue"
```

```
/note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);
```

Site 1: EcoRI; Site 2: XhoI; Directionally cloned using

Stratagene's UniZap XR cDNA cloning kit with the 5' end

at the EcoRI site. The library represents 8×10^5

independent recombinant phage. The plants were greenhouse grown."

BASE COUNT	111 a	136 c	156 g	85 t
------------	-------	-------	-------	------

ORIGIN

Query Match 78.7%; Score 331.4; DB 11; Length 488;

Best Local Similarity 99.4%; Pred. No. 2.7e-69;

Matches 332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgc 78
 |||
 Db 155 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 214

Qy 79 cgtcatggagccggttgctggcagcaacacggtagtagctggtgcccagttgagtt 138
 |||
 Db 215 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTTGAGTT 274

Qy 139 gcaaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgagggggtggcggc 198
 |||
 Db 275 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 334

Qy 199 gatctccaaaggggggaaggtanggccgaaccggtgcagcgccctgcaggaagagggttg 258
 |||
 Db 335 GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 394

Qy 259 acttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccga 318
 |||
 Db 395 ACTTACGGGATTCAACTGCCGGTGTGGGAATTGTACTGCGCACTCCACCGCTACTCCGA 454

Qy 319 caagcacgactgcaagttcgactaacggactgct 352
 |||
 Db 455 CAAGCACGACTGCAAGTTCGACTACCGGACTGCT 488

RESULT 9

BE510926/c

LOCUS BE510926 482 bp mRNA EST 07-AUG-2000
 DEFINITION 946056E05.x1 946 - tassel primordium prepared by Schmidt lab Zea
 mays cDNA, mRNA sequence.

ACCESSION BE510926

VERSION BE510926.1 GI:9732174

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 482)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946056 row: E column: 05.

FEATURES

source

Location/Qualifiers

1. .482

/organism="Zea mays"

/cultivar="OH43"

/db_xref="taxon:4577"

/clone_lib="946 - tassel primordium prepared by Schmidt

lab"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to
 inflorescence development"
 /lab_host="XL0LR"
 /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
 Site_2: XhoI; George Chuck dissected immature tassels
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA
 library in HybriZAP. Sample insert size range was 350 bp
 to 3 Kb with a 1 Kb average."

BASE COUNT 98 a 158 c 131 g 95 t
 ORIGIN

Query Match 77.1%; Score 324.8; DB 10; Length 482;
 Best Local Similarity 97.4%; Pred. No. 1e-67;
 Matches 340; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

```

Qy      73 cgacgccgtcatggagccggttggtgctggcagcaacacggtagtagctgttgcccaagt 132
      |||
Db     482 CGACGCCGTCATGGAGCCGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGT 423

Qy     133 tgagttgcaaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggt 192
      |||
Db     422 CGAGTTGCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGT 363

Qy     193 ggcggcgatctccaaaggggggaaggtanggccgaaccggtgcagcgcctgcaggaagag 252
      |||
Db     362 GGCGGCGATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAG 303

Qy     253 ggttggaacttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgcta 312
      |||
Db     302 GGTGGGCTCACGGGATTCAACTGCCGGTGTGGGAAC TTG TACTGCGCGCTCCACCGCTA 243

Qy     313 ctccgacaagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaa 372
      |||
Db     242 CTCCGACAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA 183

Qy     373 gggctaataccggtggtgaaggcagacaagctcgacaagatctaaggggg 421
      |||
Db     182 -GGCTAATCCGGTGGTGAAGGCAGACAAGCTCGACAAGATCTAGGGGGG 135
  
```

RESULT 10
 AW927909
 LOCUS AW927909 567 bp mRNA EST 30-MAY-2000
 DEFINITION 945010H04.Y1 945 - Mixed adult tissues from Walbot lab, same as 707
 (SK) Zea mays cDNA, mRNA sequence.
 ACCESSION AW927909
 VERSION AW927909.1 GI:8103259
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 567)

AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 945010 row: H column: 04.

FEATURES Location/Qualifiers
 source 1. .567
 /organism="Zea mays"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
 /tissue_type="tassel, kernal, silk, husk, root, leaf"
 /dev_stage="fully-grown"
 /lab_host="DH10B"
 /note="Organ: tassel, kernal, silk, husk, root, leaf; Vector: pGAD10; Site_1: EcoRI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."

BASE COUNT 113 a 147 c 177 g 130 t
 ORIGIN

Query Match 74.3%; Score 312.8; DB 10; Length 567;
 Best Local Similarity 97.3%; Pred. No. 7.4e-65;
 Matches 328; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

```

Qy      85 ggagccggttggttgctggcagcaacacggtagtagctggtgcccagttgagttgcaaac 144
      |||
Db      1 GGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTCGAGTTGCAAAC 60

Qy     145 aatgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggtggcggcgatctc 204
      |||
Db      61 AATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGCGATCTC 120

Qy     205 caaaggggggaaggtangggccgaaccggtgcagcgcctgcaggaagaggggttgacttac 264
      |||
Db     121 CAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGGGCTCAC 180

Qy     265 gggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccgacaagca 324
      |||
Db     181 GGGATTCAACTGCCGGTGTGGGAAC TTG TACTGCGCGCTCCACCGCTACTCCGACAAGCA 240

Qy     325 cgactgcaagttcgactaacggactgctgccaaggacgccattgccagggttaatccgg 384
      |||
Db     241 CGACTGCAAGTTGCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA-GGCTAATCCGG 299

Qy     385 tggatgaaggcagacaagctcgacaagatctaaggggg 421
  
```

Db 300 TGGTGAAGGCAGACAAGCTCGACAAGATCTAGGGGGG 336

RESULT 11
AI977903/c
LOCUS AI977903 643 bp mRNA EST 27-AUG-1999
DEFINITION 496035D05.x1 496 - stressed shoot cDNA library from Wang/Bohnert
lab Zea mays cDNA, mRNA sequence.
ACCESSION AI977903
VERSION AI977903.1 GI:5791111
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 643)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 496035 row: D column: 05.
FEATURES Location/Qualifiers
source 1. .643
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="496 - stressed shoot cDNA library from
Wang/Bohnert lab"
/tissue_type="seedling"
/dev_stage="salt stress"
/lab_host="E.coli XL Gold"
/note="Organ: shoot; Vector: pBluescriptII SK(+) XR;
Wang/Bohnert"
BASE COUNT 164 a 192 c 159 g 128 t
ORIGIN

Query Match 69.0%; Score 290.6; DB 10; Length 643;
Best Local Similarity 98.1%; Pred. No. 1.5e-59;
Matches 304; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 112 ggtagtagctgttgcccaagttgagttgcaaacaatgaacgtgcagcagccccgctgatgt 171
|||||
Db 643 GGTAGTAGCTGTTGCCCAAGTTGAGTTGCAACCAATGAACGTGCAGCAGCCCCGCTGATGT 584

Qy 172 tgccggacccagcaggggggtggcggcgatctccaaaggggggaaggtanggccgaaccg 231
|||||
Db 583 TGCCGGACCCAGCGAGGGGGTGGCGGCGATCTCCAAAGGGGGGAAGGTAGGGCCGAACCG 524

Qy 232 gtgcagcgctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaactt 291
 |||
 Db 523 GTGCAGCGCCTGCAGGAAGAGGGTTGGACTTACGGGATTCAACTGCCGGTGTGGGAACCTT 464
 Qy 292 gtactgcgcactccaccgctactccgacaagcagcactgcaagttcgactaacggactgc 351
 |||
 Db 463 GTACTGCGCACTCCACCGCTACTCCGACAAGCACGACTGCAAGTTCGACTACCGGACTGC 404
 Qy 352 tgccaaggacgccattgccaagggctaataccggtggtgaaggcagacaagctcgacaaga 411
 |||
 Db 403 TGCCAGGGACGCCATTGCCAA-GGCTAATCCGGTGGTGAAGGCAGACAAGCTCGACAAGA 345
 Qy 412 tctaaggggg 421
 |||
 Db 344 TCTAGGGGGG 335

RESULT 12

AW061851/c

LOCUS AW061851 514 bp mRNA EST 30-MAR-2000

DEFINITION 687007F12.x1 687 - Early embryo from Delaware Zea mays cDNA, mRNA sequence.

ACCESSION AW061851

VERSION AW061851.1 GI:6012414

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 514)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 687007 row: F column: 12.

FEATURES Location/Qualifiers

source

1. .514

/organism="Zea mays"

/cultivar="Illinois High Oil"

/db_xref="taxon:4577"

/clone_lib="687 - Early embryo from Delaware"

/tissue_type="embryo"

/dev_stage="14, 21, 28, and 35 days after pollination"

/lab_host="E. coli SOLR"

/note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI ; Site_2: EcoRI; Library was prepared by Statagene using the Uni-ZAP XR system (Stratagene BN937328-12). Clones were picked by a Q-bot after blue/white selection"

(ampicillin resistance - use 100 micrograms/microliter).
 Developed from a pool of equal amounts of RNA from
 developing embryos sampled at 14, 21, 28 and 35 days after
 pollination of the Illinois High Oil Maize Strain Cycle
 90. This closed strain has been selected for high oil
 concentration for 90 generations and originates from the
 1890s era open pollinated variety Burr's White"

BASE COUNT 116 a 156 c 138 g 104 t
 ORIGIN

Query Match 68.9%; Score 290; DB 10; Length 514;
 Best Local Similarity 97.7%; Pred. No. 2e-59;
 Matches 304; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

```

Qy   111  cggtagtagctgttgcccaagttgagttgcaaacaatgaacgtgcagcagcccgctgatg 170
      |||
Db   513  CGGTAGTAGCTGTTGCCCAAGTTGAGTTGCAAACAATGAACGTGCAGCAGCCCGCTGATG 454

Qy   171  ttgccggacccagcagagggggtggcggcgatctccaaaggggggaaggtanggccgaacc 230
      |||
Db   453  TTGCCGGACCCAGCGAGGGGGTGGCGGCGATCTCCAAAGGGGGGAAGGTAGGCCCGAACC 394

Qy   231  ggtgcagcgcctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaact 290
      |||
Db   393  GGTGCAGCGCCTGCAGGAAGAGGGTTGGACTTACGGGATTCAACTGCCGGTGTGGGA ACT 334

Qy   291  tgtactgcgcaactccaccgctactccgacaagcagcactgcaagttcgactaacggactg 350
      |||
Db   333  TGTACTGCGCACTCCACCGCTACTCCGACAAGCAGCACTGCAAGTTCGACTACCGGTCTG 274

Qy   351  ctgccaaggacgccattgccaaagggctaatccggtggtgaaggcagacaagctcgacaag 410
      |||
Db   273  CTGCCAGGGACGCCATTGCCAA-GGCTAATCCGGTGGTGAAGGCAGACAAGCTCGACAAG 215

Qy   411  atctaaggggg 421
      |||
Db   214  ATCTAGGGGGG 204
  
```

RESULT 13

AI649645

LOCUS AI649645 527 bp mRNA EST 30-APR-1999
 DEFINITION 486077B07.y1 486 - leaf primordia cDNA library from Hake lab Zea
 mays cDNA, mRNA sequence.

ACCESSION AI649645

VERSION AI649645.1 GI:4730479

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 527)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University

JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 486077 row: B column: 07.

FEATURES Location/Qualifiers
 source 1. .527
 /organism="Zea mays"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone_lib="486 - leaf primordia cDNA library from Hake
 lab"
 /tissue_type="leaf primordia"
 /dev_stage="P7-P11 leaf"
 /lab_host="E.coli XL1-Blue MFR"
 /note="Organ: shoot; Vector: Lambda zap; Hake lab cDNA
 library."

BASE COUNT 117 a 151 c 169 g 90 t
 ORIGIN

Query Match 68.3%; Score 287.4; DB 10; Length 527;
 Best Local Similarity 99.0%; Pred. No. 8.5e-59;
 Matches 299; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```

Qy      19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgc 78
      |||
Db      226 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 285

Qy      79 cgtcatggagccggttggttgctggcagcaacacggtagtagctggtgcccagttgagtt 138
      |||
Db      286 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTTGAGTT 345

Qy      139 gcaaacaatgaacgtgcagcagcccgctgatggtgcccggacccagcgaggggggtggcggc 198
      |||
Db      346 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 405

Qy      199 gatctccaaaggggggaaggtangggccgaaccggtgcagcgccctgcaggaagaggggttg 258
      |||
Db      406 GATCTCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 465

Qy      259 acttacgggattcaactgcccgtgtgggaacttgactgcgcactccaccgctactccga 318
      |||
Db      466 ACTTACGGGATTCAACTGCCGG-GGGGAACTTGTA TCGGCACTCCACCGCTACTCCGA 524

Qy      319 ca 320
      ||
Db      525 CA 526
  
```

RESULT 14
 BE129734/c
 LOCUS BE129734 599 bp mRNA EST 21-JUN-2000

DEFINITION 946003G07.X1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.
 ACCESSION BE129734
 VERSION BE129734.1 GI:8577097
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 599)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946003 row: G column: 07.
 FEATURES Location/Qualifiers
 source 1..599
 /organism="Zea mays"
 /cultivar="OH43"
 /db_xref="taxon:4577"
 /clone_lib="946 - tassel primordium prepared by Schmidt lab"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to inflorescence development"
 /lab_host="XL0LR"
 /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
 BASE COUNT 149 a 182 c 152 g 116 t
 ORIGIN

Query Match 65.7%; Score 276.8; DB 10; Length 599;
 Best Local Similarity 97.0%; Pred. No. 2.9e-56;
 Matches 292; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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Qy 121 tgttgcccaagttgagttgcaaacaatgaacgtgcagcagcccgctgatgttgccggacc 180
    |||
Db 599 TGTTGCCCAAGTCGAGTTGCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACC 540

Qy 181 cagcgaggggggtggcggcgatctccaaaggggggaaggtanggccgaaccggtgcagcgc 240
    |||
Db 539 CAGCGAGGGGGTGGCGGCGATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGC 480

Qy 241 ctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaacttgactgcgc 300
    |||
  
```

```

Db      479 CTGCAGGAAGAGGGTTGGGCTCACGGGATTCAACTGCCGGTGTGGGAACCTGTACTGCGC 420
Qy      301 actccaccgctactccgacaagcacgactgcaagttcgactaacggactgctgccaagga 360
        |||
Db      419 GCTCCACCGCTACTCCGACAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGA 360
Qy      361 cgccattgccaaggggctaatccggtggtgaaggcagacaagctcgacaagatctaagggg 420
        |||
Db      359 CGCCATTGCCAA-GGCTAATCCGGTGGTGAAGGCAGACAAGCTCGACAAGATCTAGGGGG 301
Qy      421 g 421
        |
Db      300 G 300

```

RESULT 15

W99253

LOCUS W99253 660 bp mRNA EST 17-JUL-1996

DEFINITION EST01 Glucose-starved maize root tip cDNA library Zea mays cDNA clone MZ2B1 3' similar to Phaseolus vulgaris PVPR3, mRNA sequence.

ACCESSION W99253

VERSION W99253.1 GI:1432180

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 660)

AUTHORS Couee, I. and Chevalier, C.

TITLE Maize root cDNAs

JOURNAL Unpublished (1996)

COMMENT Contact: Couee I

Station d'amelioration des arbres forestiers

Institut National de la Recherche Agronomique

F-45160 Ardon, France

Fax: 33-38417879

Email: couee@orleans.inra.fr

Similarity determined by BLASTX.

FEATURES Location/Qualifiers

source 1. .660

/organism="Zea mays"

/cultivar="DEA"

/db_xref="taxon:4577"

/clone="MZ2B1"

/clone_lib="Glucose-starved maize root tip cDNA library"

/tissue_type="3-mm-long tip"

/note="Organ: Primary root; Vector: Lambda ZAPII; cDNA library from poly(A)+ mRNA of 24-h glucose-starved maize root tips, as described in Chevalier, C., Bourgeois, E., Pradet, A., Raymond, P. (1995) Plant Molecular Biology Volume 28 Pages 473-485"

BASE COUNT 142 a 165 c 196 g 154 t 3 others

ORIGIN

Query Match 62.8%; Score 264.2; DB 11; Length 660;

Best Local Similarity 95.1%; Pred. No. 3e-53;
Matches 292; Conservative 0; Mismatches 12; Indels 3; Gaps 2;

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Qy 113 gtagtagctgttgcccaagttgagttgcaaacaatgaacgtgcagcagcccgctgatgtt 172
      |||
Db 1 GTAGTAGCTGTTGCCCAAGTCGAGTTGCAAACAATGAACGTGCAGCAGCCCGCNGATGTT 60

Qy 173 gccggacccagcgaggggg--tggcggcgatctccaaaggggggaaggtanggccgaacc 230
      |||
Db 61 GCCGGACCCAGCGAGGGGGGTTGGCGGCGATCTCCAAAGGGGGGAAGGTAGGGCCGAACC 120

Qy 231 ggtgcagcgcctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaact 290
      |||
Db 121 GGTGCAGCGCCTGCAGGAAGAGGGTTGGGCTCACGGGATTCAACTGCCGGTGTGGGAACT 180

Qy 291 tgtactgcgcactccaccgctactccgacaagcacgactgcaagttcgactaacggactg 350
      |||
Db 181 TGTACTGCNCCCTCCACCGCTACTCCGACAAGCACGACTGCAAGTTCGACTACCGGACTG 240

Qy 351 ctgccaaggacgccattgccaaagggctaatccgggtggtgaaggcagacaagctcgacaag 410
      |||
Db 241 CTGCCAGGGATNCCATTGCCAA-GGCTAATCCGGTGGTGAAGGCAGACAAGCTCGACAAG 299

Qy 411 atctaag 417
      |||
Db 300 ATCTAGG 306
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Job time: 18128 sec